

# Sugar Charles Carlo SEQUENCE LISTING

<110>	Rouquier	, Sylvie
	Giorgi,	Dominique

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- cag gtc tat ttc tcc atg ttt ttt cct att ctg ggc aca cta ctc ctg Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Gly Thr Leu Leu Leu 45 35
- 193 acc gtg atg gcc tat gac cgg ttt gtg gcc gtc tgc cac ccc ctg cac Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His
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- aca cat cta acc ttc tgt aaa gat ttt gaa att cca cat ttt ttc tgc 337 Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys 105
- 385 gaa ctg aca cat atc ctc cag ctg gcc tgc tct gat acc ttc ctg aac Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn 125 115



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125 120 . 115

Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu

Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys 155

Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser 170 165

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  - Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
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Val Met Tyr Thr Val Val Thr Pro

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Tyr Thr Val Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Leu Gly 70

Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr Leu Thr Val 90

Leu Arg Leu Ser Phe Cys Ile Lys Met Glu Ile Pro His Phe Phe Cys 105 100

Asp Leu Pro Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn 125

Asn Val Val Ile Tyr Phe Ala Thr Gly Ile Leu Ala Val Ile Pro Phe

Thr Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Phe Ser Val Leu Arg

Ile Ser Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser 170 165

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aca ca Thr Hi	at cta is Leu	acc Thr 100	Phe	tgt Cys	aaa Lys	gat Asp	ttt Phe 105	gaa Glu	att Ile	cca Pro	cat His	ttt Phe 110	ttc Phe	tgc Cys	337
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Ser Leu Gln Thr Arg Ser Lys Ala Ile Ser Tyr Pro Cys Cys Leu Thr
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Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser Ile Ile Ile
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Ala Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
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Tyr Ala Thr Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Gly Val
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Pro Trp Ala Phe Ser Cys Phe Ile Ser Leu Thr His Ile Leu Leu Met
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Ala Arg Leu Val Phe Cys Gly Ser His Glu Val Pro His Tyr Phe Cys
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His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile Gly Val Tyr
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cag Gln	atg Met	tgc Cys 35	ttt Phe	ttc Phe	ata Ile	ttc Phe	ttt Phe 40	gcg Ala	gga Gly	ctg Leu	gat Asp	atc Ile 45	ttt Phe	atg Met	ctg Leu	145
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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His

Tyr Thr Val Thr Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala

Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Met Val

Leu His Leu Ser Phe Cys Ala Asp Leu Glu Ile Pro His Phe Phe Cys 100

Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn 120

Asp Met Val Met Tyr Leu Ala Ser Ala Leu Leu Gly Gly Gly Ala Leu 135

Ser Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Gly 155

Thr Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser

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# Val Met Tyr Thr Val Val Thr Pro 210 215

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Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn
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170

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481

tgt ctg gtt ctt ttg tct tac atc cgg atc atc tcc acc atc tta aag

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Ser	Trp	Val	. Ser	Gly 85	, Ser	· Ile	Asn	Sei	Leu 90	ı Met	: His	Thr	Thr	95	. Thr		
Phe	Gln	ı Leı	Pro		. Cys	: Thr	Asr	10!	s Phe	e Ile	e Asr	n His	: Ile 110	Phe	e Cys		
Glu	Ile	e Lei 115		a Val	l Il€	e Arg	120	ı Ala	a Cys	s Val	L Ası	Th:	Sei	s Sei	Asn		
Glu	Va]		r Ile	e Met	z Val	1 Ser		c Il	e Vai	l Lei	ı Lei 140	ı Met	Th:	r Pro	) Leu		

Cys Leu Val 145	Leu Leu	Ser 7	Tyr II	le Ai	rg I		le S 55	Ser I	hr :	[le ]	Leu	Lys 160	
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His Leu Thr	Val Val 180	Ala I	Leu C	ys T	yr G 85	ly M	iet A	Ala J	le	Phe 190	Thr	Tyr	
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Leu Leu Ile Leu Cys Ser Tyr Thr Arg Ile Ala Ala Ile Leu Lys 155

Ile Pro Ser Ala Lys Gly Lys Asn Lys Ala Phe Ser Thr Arg Ser Ser

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Gln Val Tyr Phe Ser Met Leu Phe Pro Ile Leu Asp Thr Leu Leu Leu
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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
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 Tyr Met Ile Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Ile Phe Val
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Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys 150

Met Ser Ser Ser Gly Gly Lys Gln Lys Ala Leu Ser Thr Cys Gly Ser 170

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Gln Va	l Tyr 35	Phe	e Ser	Met	Leu	Phe 40	Pro	) Ile	Leu	Asp	Thr 45	Leu	Leu	Leu	
Thr Va 50	l Met	: Ala	ı Tyr	Asp	Arg 55	Phe	e Val	. Ala	lle	Cys 60	Leu	. Pro	Leu	His	
Tyr Me	t Ile	e Ile	e Met	Asr 70	Pro	Arg	, Lev	ı Cys	Gly 75	Leu	ı Lev	Ile	. Phe	val 80	

The Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met 90

Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys 100

Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125

Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val Phe Pro Leu 130 135 140

Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys 145 150 155 160

Met Ser Ser Ser Gly Gly Lys Gln Lys Ala Leu Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His 180  $\,$  185  $\,$  190  $\,$ 

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						cga Arg 55										193
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tca Ser	tac Tyr	tct Ser	tgg Trp	999 61y 85	ata Ile	gtc Val	tgt Cys	ttc Phe	ctg Leu 90	aca Thr	ctt Leu	acc Thr	tac Tyr	ttt Phe 95	cta Leu	289
ctg Leu	gaa Glu	tta Leu	tcc Ser 100	ttc Phe	aga Arg	gga Gly	aat Asn	aat Asn 105	atc Ile	att Ile	aat Asn	aac Asn	ttt Phe 110	gtc Val	tgt Cys	337
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atg Met 145	atg Met	att Ile	ttc Phe	act Thr	tcc Ser 150	tat Tyr	gct Ala	ttc Phe	att Ile	ttt Phe 155	atc Ile	act Thr	gtc Val	atg Met	aag Lys 160	481
atg Met	cct Pro	tcc Ser	act Thr	999 Gly 165	Gly 999	cgc Arg	aag Lys	aaa Lys	gcg Ala 170	ttc Phe	tcc Ser	acg Thr	tgt Cys	gcc Ala 175	tcc Ser	529
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- Gln Phe Phe Leu Val Cys Ile Phe Val Gly Thr Glu Thr Phe Met Leu
- Ala Val Met Ala Tyr Asp Arg Cys Val Ala Val Cys Asn Pro Leu Leu 60 50 55
- Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ser Leu Leu Val Ala Thr
- Ser Tyr Ser Trp Gly Ile Val Cys Phe Leu Thr Leu Thr Tyr Phe Leu
- Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe Val Cys
- Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Tyr Val Ser
- Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Leu 130
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- Met Pro Ser Thr Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ala Ser 170 165
- His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr 185
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                                                                      300
                                                                      360
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540

600 650

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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His

Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Ala

Ser Trp Ile Val Gly Val Leu Asn Ser Met Leu Gln Ser Leu Met Val

Leu Pro Leu Pro Phe Cys Thr His Met Glu Ile Pro His Phe Phe Cys 100

Glu Ile Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn 120 115

Asp Ile Val Met Tyr Phe Ala Val Ala Leu Leu Gly Gly Pro Leu 135 130

Asn Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 155

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 170

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Val Met Tyr Thr Val Val Thr Pro

215

His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr

577

ctg agt tot gct gtg acc cat tot toe cag age age tee atg gcc tea Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser Met Ala Ser 200

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Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His

Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu Val Leu Ala

Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Val Leu Leu Met 90

Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys 100

Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr Leu Leu Asn

Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val

Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg

Thr Ser Ser Thr Lys Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser 170 165

His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr 180 185 190

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Val Met Tyr Ala Met Val Thr Pro 210 215

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Ala Gly Ile Phe Tyr Ser Tyr Phe Lys Ile Leu Cys Cys Ile Cys Ser

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cac His	ctc Leu	tca Ser	gtt Val 180	gtc Val	tcc Ser	tta Leu	ttt Phe	tat Tyr 185	tgt Cys	aca Thr	ggc Gly	gta Val	ggt Gly 190	gtg Val	tac Tyr	577
ctt Leu	agt Ser	tct Ser 195	gct Ala	gca Ala	acc Thr	cat His	aac Asn 200	tca Ser	ctc Leu	tca Ser	aat Asn	gct Ala 205	gca Ala	gcc Ala	tca Ser	625
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			100					105					110	)	Cys	
		115					120	)				125	5		Lys	
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                                                                                97
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Asn Ile Gln Ala Arg Ile Lys Asp Ile Ser Tyr Met Gly Cys Leu Thr
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Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr Phe Leu Leu
                                                                                193
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 Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 tac acg gtc atc atg aac ccc tgc ctc tgt ggc ctc ctg gtt ctg gca
Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu Val Leu Ala
                                                                                241
                        70
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 tot tgg tto atc att tto tgg tto too etg gtt cat att cta etg atg
                                                                                289
 Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile Leu Leu Met
 aag aag ttg acc ttc tcc aca ggc act gag att ccg cat ttc ttc tgt
                                                                                337
 Lys Lys Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys
                                     105
               100
 gaa ccg gct cag gtc ctc aag gtg gcc tgc tct aac acc ctc ctc aat
Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr Leu Leu Asn
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115 120 125

115 120 125	
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gct ggg atc ctc ttc tcc tac tct cag att gtc tcc tcc tta atg aga 481 Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg 145 150 155 160	
acg tcc tcc acc gag ggc aag tac aaa gcc ttt tcc acg ctg tgg atc 529 Thr Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr Leu Trp Ile 165 170 175	
tcc ctc tgt gtg gtc tcc ttg ttc tat gga aca gga ctt ggg gtc tat 577 Ser Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr 180 185 190	
ctg agt tct gct gtg acc cac tct tcc cag agc agc tcc atg gcc tca 625 Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser Met Ala Ser 195 200 205	
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Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60	
Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu Val Leu Ala 65 70 75 80	
The The The The Cor Low Val Hig The Lew Met	
Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile Leu Leu Met 85 90 95	

Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr Leu Leu Asn 125 115	
Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val 135 130  Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val 140	
Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg 160 155 145	
Thr Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr Leu Trp Ile  175  165	
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tggaggcatg gaagagagac atgctcctga gtgtgatggc ctatgaccgg tttgtagcca
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                                                                      360
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aat ata ctg aca cag aac aaa ttc ata aca tat gca ggc tgt ctc ggt
                                                                       97
Asn Ile Leu Thr Gln Asn Lys Phe Ile Thr Tyr Ala Gly Cys Leu Gly
                                                                      145
cag att ttt ttt ttc act tca ttt gga tgc ctg gac aat tta ctc ttg
Gln Ile Phe Phe Phe Thr Ser Phe Gly Cys Leu Asp Asn Leu Leu
act gtg atg gcc tat gac cgc ttc gtg gcc atc tgt cac ccc ctg cac
                                                                      193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 tat acg gtc atc atg aac ccc cgg ctc tgt gga ctg ctg gtt ctg ggg
                                                                       241
 Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Gly
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Leu Arg Leu Ser Phe Cys Thr Lys Met Glu Ile Pro His Phe Phe Cys
Asp Leu Leu Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn
Asn Val Val Ile Tyr Phe Ala Thr Gly Val Leu Gly Val Ile Pro Phe
Thr Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Val Phe Ser Ile Leu Arg
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Ile Ser Ser Ala Gly Arg Lys His Lys Ala Phe Ser Thr Cys Gly Ser
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His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Phe Gly Val Tyr
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cag atg tgc ttt gtt ctg ggt tct gct acg ttg gaa aat ttt ctc ctg
Gln Met Cys Phe Val Leu Gly Ser Ala Thr Leu Glu Asn Phe Leu Leu
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tcc ctg tc Ser Leu Se	att ago Ile Ser 85	atc atg	gac ac Asp Th	c ctg r Leu 90	ctc Leu	cac His	gat Asp	ctg Leu	atg Met 95	gtc Val	289
ttg cgg cte Leu Arg Le	g tcc ttc ı Ser Phe 100	tgc aca Cys Thr	cac ct His Le 10	u Glu	ata Ile	ccc Pro	ctc Leu	ttc Phe 110	ttc Phe	tgc Cys	337
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aac ctc tt Asn Leu Le 130	g ata tat u Ile Tyr	ttt gca Phe Ala 135	gct gg Ala Gl	c gtg y Val	ttg Leu	gga Gly 140	ggt Gly	gtt Val	cct Pro	ctg Leu	433
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atg gca tc Met Ala Se	a gca agt r Ala Ser 165	: Gly Lys	tat aa Tyr Ly	a gct s Ala 170	Phe	tcc Ser	acc Thr	tgt Cys	ggc Gly 175	tct Ser	529
cac ctc tc His Leu Se	g gtt gtg r Val Val 180	g too ttg L Ser Leu	ctc to Leu Ty 18	r Gly	aca Thr	ggt Gly	ttg Leu	999 Gly 190	gtg Val	tac Tyr	577
atc agt to Ile Ser Se 19	r Ala Phe	atg cac Met His	tct co Ser Pi 200	c agg	acg Thr	atg Met	gca Ala 205	gtg Val	gct Ala	tca Ser	625
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Ser Leu Ser Ile Ser Ile Met Asp Thr Leu Leu His Asp Leu Met Val

Leu Arg Leu Ser Phe Cys Thr His Leu Glu Ile Pro Leu Phe Phe Cys

Glu Val Val Gln Val Ile Lys Leu Ala Cys Ser Asp Thr Leu Ile Asn 120 115

Asn Leu Leu Ile Tyr Phe Ala Ala Gly Val Leu Gly Gly Val Pro Leu 135

Ser Gly Ile Ile Phe Ser Tyr Thr Gln Ile Ala Ser Ser Val Leu Arg 155 145

Met Ala Ser Ala Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser

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180

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                                                                    600
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Tyr Met Val Ile Met Asn Pro Arg Phe Cys Ala Leu Leu Val Leu Met 65 70 75 80

Ser Trp Phe Ile Met Ser Leu Val Ala Leu Val His Val Leu Leu Ile 85 90 95

Leu Arg Leu Thr Phe Ser Leu Glu Thr Glu Ile Pro His Phe Ser Cys 100 105 110

Glu Val Ala Gln Ile Leu Lys Val Ala Arg Ser Asp Thr Phe Phe Asn 115 120 125

Asn Ile Cys Leu Tyr Leu Ser Ala Val Leu Leu Gly Val Phe Pro Val 130 135 140

Met Gly Ile Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Leu Met Arg 145 150 155 160

Met Ser Ser Thr Ser Ala Lys Asn Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175

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155

Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser 170

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<222 <4(Phe 1 Asr	:3> :00> : Ser : Val : Met	Taxo 71 Asp Glr Asp 35	n =  Ile Thr 20 Phe	Cys 5 His	Leu Ser Val	Val Lys Leu Arg	Ser Val Phe 40	Thr Ile 25 Val	Thr 10 Ser Gly	Val Tyr Leu	Ala Asp Cys	Gln Gly Ser 45	Met Cys 30 Phe	Leu 15 Val Leu	Val Thr	= AF127	862
<222 <40 Phe 1 Ass Gli Th:	23> 00> e Ser n Val n Met r Val 50	Taxo 71 Asp Glr 35 Met	n = Ile Thr 20 Phe	Cys 5 His	Leu Ser Val Asp	Val Lys Leu Arg 55	Ser Val Phe 40 Phe	Thr Ile 25 Val	Thr 10 Ser Gly Val	Val Tyr Leu Gly 75	Ala Asp Cys 60	Gly Ser 45 His	Met Cys 30 Phe	Leu 15 Val Leu Leu	Val Thr Leu His	= AF127	862
<222 <4(Phe 1 Asi Gli Th:	3> 00> e Ser n Val n Met r Val 50 r Ala	Taxo 71 Asp Glr 35 Met	n = Ile Thr 20 Phe Ala	Cys 5 His Phe Tyr Met	Leu Ser Val Asp Asr 70	Leu Leu Arc 55	Ser Val Phe 40 Phe Arc	Thr Ile 25 Val	Thr 10 Ser Gly Val Cys r Let 90	Val Tyr Leu Gly 75	Ala Asp Cys 60 Leu	Gly Ser 45 His	Met Cys 30 Phe Pro	Leu 15 Val Leu Leu 1 Val 95	Val Thr Leu His	= AF127	862

Asp Met Val Met Tyr Phe Ser Ala Leu Leu Leu Gly Gly Ser Leu

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Val Arg Ala 155

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 165

His Leu Ala Val Val Ser Leu Phe Tyr Cys Thr Ser Leu Gly Val Tyr 185 180

Leu Ser Ser Ala Ala Thr His Asn Ser His Ser Ser Ala Thr Ala Ser 200 195

Val Met Tyr Thr Val Val Thr Pro

<210> 72

<211> 642

<212> DNA

Eulemur rubriventer <213>

<220>

misc\_feature <221>

(1)..(642) <222>

Taxon = 34829; gene = EFU84; pseudogene; Accession DDBJ/EMBL/ GenBank <223> = AF127863

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<sup>&</sup>lt;210> 73

<sup>&</sup>lt;211> 652

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Eulemur fulvus

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<223> Taxon = 13515; gene = EFU86; pseudogene; Accession DDBJ/EMBL/GenBank
= AF127864
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acagagcaaa gtcatatcct acgcaggctg cgtcacccag atggactttt tcatactctt
                                                                      120
tgcagggttg gatatcttta tgctgatcat gatggcctat gaccggtttg gggccatctg
                                                                      180
tcacccactg cagtacacgg tcatcatgaa ccccaggete tgtgggetge tggttgtggt
                                                                      240
gccctggatc ttgagtgacc tgaattcctt gttacaaagc ttaatggtgt tgtcactgtc
                                                                      300
cttttgtaga cacttggaaa teeteaettt ttetgtgaae ttaateaggt tgteeaeett
                                                                      360
gcctgttctg aaaccttctt taatgacatg gtgatgtatc tgatatctgt ggtgctgggt
                                                                      420
ggtggttccc tggctgggac tctttattct ttcttactgc agaatagttt gctccatacg
                                                                      480
tgcaacgtcc tcagctcagg ggaagtataa agcatttccc acctgtgcat ctcacctctc
                                                                      540
agttgtctcc ttatcttcct gcacaatcct aggggtgtac ctcagctctg ctgctaccca
                                                                      600
                                                                      652
gaattcgtgc tccagtgcag tagccttggt ggtgtacacg gtggtcactc cc
       74
<210>
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       649
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       DNA
       Eulemur fulvus
<213>
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<222>
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                                                                        49
  Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro Lys Met Leu Val
aac att gaa aca cac agc aaa gac atc tcc tac atg gga tgc ctc act
                                                                        97
Asn Ile Glu Thr His Ser Lys Asp Ile Ser Tyr Met Gly Cys Leu Thr
                                                                       145
cag atg tat ttt ttc atg att ttt gct gga ctg gat aat ttc ctc ctg
Gln Met Tyr Phe Phe Met Ile Phe Ala Gly Leu Asp Asn Phe Leu Leu
                             40
                                                                       193
 act gtg atg gcc tat gac cgg ttt gtg gcc atc tgc cac ccc tta cac
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
                                             60
                                                                       241
 tac acg gtc atc atg agt ccc cgc ttc tgt gcc ctc ctg gtt ctc ata
 Tyr Thr Val Ile Met Ser Pro Arg Phe Cys Ala Leu Leu Val Leu Ile
                                         75
                     70
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tct tgg ttc atc atg acc ctg gtt gcc ctg gtt cat gta cta ctg ata Ser Trp Phe Ile Met Thr Leu Val Ala Leu Val His Val Leu Leu Ile 85 90 95	289
ttg agg ctg acc ttc tct tta gaa act gaa atc cca cat ttc ttc tgt Leu Arg Leu Thr Phe Ser Leu Glu Thr Glu Ile Pro His Phe Phe Cys 100 105 110	337
gac ctg gct cag att ctc gag gtg gcc cac tct gat acc ctc atc aat Asp Leu Ala Gln Ile Leu Glu Val Ala His Ser Asp Thr Leu Ile Asn 115	385
aac atc tgc atg tac ttg tcg act gtg ttg ctg ggc gtg ttt cct gtc Asn Ile Cys Met Tyr Leu Ser Thr Val Leu Leu Gly Val Phe Pro Val 130 135 140	433
acg ggg atc ctc ttc tcc tac tct aaa att gtc tcc tcc tta atg agg Thr Gly Ile Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Leu Met Arg 145	481
atg tcc tcc act gca ggc aag aag aaa gca ttt tcc acc tgt ggg tct Met Ser Ser Thr Ala Gly Lys Lys Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175	529
cac ctc tct gtg gtc tgc ttg ttc tgc gga aca gga gtt ggg gtc tat His Leu Ser Val Val Cys Leu Phe Cys Gly Thr Gly Val Gly Val Tyr 180 185 190	577
ctc agt tct gct gtg acc cct tct tcc cag agc agc agc att gcc tca Leu Ser Ser Ala Val Thr Pro Ser Ser Gln Ser Ser Ser Ile Ala Ser 195 200 205	625
gtg atg ttc acg gtg gtc acc ccc Val Met Phe Thr Val Val Thr Pro 210 215	649
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Asn Ile Glu Thr His Ser Lys Asp Ile Ser Tyr Met Gly Cys Leu Thr 20 25 30	
Gln Met Tyr Phe Phe Met Ile Phe Ala Gly Leu Asp Asn Phe Leu Leu 35 40 45	
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His	

Ser Trp Phe Ile Met Thr Leu Val Ala Leu Val His Val Leu Leu Ile 90 85

75

Leu Arg Leu Thr Phe Ser Leu Glu Thr Glu Ile Pro His Phe Phe Cys 105

Asp Leu Ala Gln Ile Leu Glu Val Ala His Ser Asp Thr Leu Ile Asn 120 115

Asn Ile Cys Met Tyr Leu Ser Thr Val Leu Leu Gly Val Phe Pro Val 130 135

Thr Gly Ile Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Leu Met Arg 150 145

Met Ser Ser Thr Ala Gly Lys Lys Lys Ala Phe Ser Thr Cys Gly Ser

His Leu Ser Val Val Cys Leu Phe Cys Gly Thr Gly Val Gly Val Tyr 190

Leu Ser Ser Ala Val Thr Pro Ser Ser Gln Ser Ser Ser Ile Ala Ser 205 200

Val Met Phe Thr Val Val Thr Pro 210

<210> 76

<211> 646

DNA <212>

<213> Macaca sylvanus

<220>

65

<221> misc\_feature

<222> (1)..(646)

<223> Taxon = 9546; gene = MSY1; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127866

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gtcc	tcca	.cc g	aggg	caag	t go	aaag	cctt	ttc	cacc	tgt	gggt	ctca	CC L	etgt	grggr	540
ctcc	ttgt	tc t	atgg	aaca	g ga	.cttg	gggt	cta	tctc	agt	tctg	ctgt	ga c	ccat	tcttc	600
ccag	agca	gc t	ccat	ggcc	t ca	.gtga	tgta	cac	catg	gtc	accc	CC				646
<210> 77 <211> 649 <212> DNA <213> Macaca sylvanus																
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<220> <221> CDS <222> (2)(649) <223> Product = olfactory receptor																
<400> 77 c ttc gta gac gtc tgt ttt gtg tcc acc act gtc ccg aag atg ctg gtg Phe Val Asp Val Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val 1 5 10																
aac Asn	atc Ile	cag Gln	aca Thr 20	cag Gln	aac Asn	aaa Lys	gtc Val	atc Ile 25	acc Thr	tat Tyr	gca Ala	ggc Gly	tgc Cys 30	atc Ile	agc Ser	97
cag Gln	atg Met	tgc Cys 35	ttt Phe	ttc Phe	ata Ile	ttc Phe	ttt Phe 40	gca Ala	gga Gly	ttg Leu	gac Asp	atc Ile 45	ttt Phe	atg Met	ctg Leu	145
acc Thr	gtg Val 50	atg Met	gcc Ala	tac Tyr	gac Asp	agg Arg 55	ttt Phe	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	cac His	193
tac Tyr 65	acg Thr	gtc Val	acc Thr	atg Met	aac Asn 70	ccc Pro	agg Arg	ctc Leu	tgt Cys	gga Gly 75	ctg Leu	ctg Leu	gtt Val	ctg Leu	gcg Ala 80	241
tcc Ser	tgg Trp	atc Ile	atg Met	agt Ser 85	gcc Ala	ctg Leu	aat Asn	tct Ser	tca Ser 90	ttg Leu	caa Gln	agc Ser	tta Leu	atg Met 95	gta Val	289
ttg Leu	cac His	ctt Leu	tcc Ser 100	ttc Phe	tgt Cys	gca Ala	gac Asp	ttg Leu 105	gaa Glu	att Ile	ccc Pro	cac His	ttt Phe 110	ttc Phe	tgt Cys	337
gaa Glu	ctt Leu	aat Asn 115	cag Gln	gtc Val	atc Ile	cac His	ctt Leu 120	acc Thr	tgt Cys	tct Ser	gac Asp	act Thr 125	ttt Phe	ctt Leu	aat Asn	385
gac Asp	atg Met 130	gtg Val	atg Met	tat Tyr	ttg Leu	tca Ser 135	gct Ala	gtg Val	ctg Leu	ctg Leu	ggt Gly 140	Gly aaa	gga Gly	tgt Cys	ctc Leu	433
att Ile 145	GJA aaa	atc Ile	ctt Leu	tac Tyr	tct Ser 150	tac Tyr	tct Ser	aag Lys	atc Ile	gtc Val 155	tcc Ser	tct Ser	ata Ile	cat His	gca Ala 160	481
atc Tle	tca Ser	tca Ser	gtt Val	cag Gln	999 Glv	aag Lvs	tac Tvr	aag Lvs	gca Ala	ttt Phe	tcc Ser	acc Thr	tgt Cys	gca Ala	tct Ser	529

165 170 175

cac ctc tcg gtt gtc tcc tta ttt tat tgt aca atc cta ggt gtg tac
His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Ile Leu Gly Val Tyr
180

ctt agt tct gct gca acc cac agc tca cac gca agt gct gca gtc tcg
Leu Ser Ser Ala Ala Thr His Ser Ser His Ala Ser Ala Ala Val Ser
195

577

625

625

gtg atg tac act gtg gtt acc ccc

Val Met Tyr Thr Val Val Thr Pro
210

215

<210> 78 <211> 216

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<213> Macaca sylvanus

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<222> (1)..(649)

<223> Taxon = 9546; gene = MSY12; Accession DDBJ/EMBL/GenBank = AF127867

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Gln Met Cys Phe Phe Ile Phe Phe Ala Gly Leu Asp Ile Phe Met Leu 35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Thr Val Thr Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala 70 75 80

Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Met Val 85 90 95

Leu His Leu Ser Phe Cys Ala Asp Leu Glu Ile Pro His Phe Phe Cys 100 105 110

Glu Leu Asn Gln Val Ile His Leu Thr Cys Ser Asp Thr Phe Leu Asn 115 120 125

Asp Met Val Met Tyr Leu Ser Ala Val Leu Leu Gly Gly Cys Leu 130 140

Ile Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile His Ala 145 150 155 160

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Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
165 170 175
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His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Ile Leu Gly Val Tyr 180 185 190

Leu Ser Ser Ala Ala Thr His Ser Ser His Ala Ser Ala Ala Val Ser 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

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<210> 79
<211> 649
<212> DNA
<213> Macaca sylvanus
<220>
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<222> (1)..(649)
<223> Taxon = 9546; gene = MSY16; Accession DDBJ/EMBL/GenBank = AF127868
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<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor
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                                                                       49
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                                       10
aac atc cag gcg cag agc aat gcc atc agc tat gca ggc tgc atc tcc
                                                                        97
Asn Ile Gln Ala Gln Ser Asn Ala Ile Ser Tyr Ala Gly Cys Ile Ser
            20
cag atg tat ttt ttc atg gtt ttt gga ggc ata gac aca ttt ctc ctc
                                                                       145
Gln Met Tyr Phe Phe Met Val Phe Gly Gly Ile Asp Thr Phe Leu Leu
acc gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac ccc ctg tac
                                                                       193
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr
                        55
tac cct gtc att atg aac ccc cgc ctc tgt ggc ctg ctg gtt ctt gtg
                                                                       241
Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val
                     70
 tee tgg tte etc age ttg tea tae tee etg ate eag agt etg ttg atg
                                                                       289
 Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
                                     90
                 85
 ctg cag ttg tee ttt tgc acc agt tgg gtc att cag cac ttt tac tgc
                                                                       337
Leu Gln Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys
             100
                                                                       385
 gag ctt gct cag gcc ctc acg ctt gcc tgc tca gac aca cac atc aat
 Glu Leu Ala Gln Ala Leu Thr Leu Ala Cys Ser Asp Thr His Ile Asn
                             120
                                                                       433
 tac atc ctg ctc tac gtg gtg acc ggc ctt ctg ggt ttt gtg ccc ttc
 Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu Gly Phe Val Pro Phe
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130 135 140

	130					135					140						
tc Se: 14	a gga r Gly 5	atc Ile	ctt Leu	Phe	tcc Ser 150	tac Tyr	acc Thr	caa Gln	att Ile	gtc Val 155	tcc Ser	tcc Ser	atc Ile	ctg Leu	aga Arg 160		481
at Il	c tca e Ser	tcc Ser	aca Thr	gat Asp 165	ggg Gly	aaa Lys	cac His	aaa Lys	gcc Ala 170	ttt Phe	tct Ser	aac Asn	tgc Cys	gga Gly 175	tct Ser		529
ca Hi	t ctg s Leu	tct Ser	gtg Val 180	gtt Val	ttt Phe	tta Leu	ttc Phe	tat Tyr 185	G1 y	aca Thr	ggc Gly	ctt Leu	ggt Gly 190	gtg Val	tat Tyr		577
ct Le	t agt u Ser	tcc Ser 195	Asn	gca Ala	tcg Ser	tcc Ser	tct Ser 200	tcc Ser	tgg Trp	cgg Arg	ggc Gly	atg Met 205	gtg Val	gcc Ala	tcg Ser		625
gt Va	c atg l Met 210	Tyr	act Thr	gtg Val	gtc Val	acc Thr 215	ccc Pro										649
<2 <2	10> 11> 12> 13>	80 216 PRT Maca	ca s	ylvar	nus												
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< 4 Le 1	00> eu Ala	80 a Asp	) Ile	Gly 5	Phe	Thr	Ser	Thr	Thr 10	Val	Pro	Lys	Met	Leu 15	Val		
As	sn Il	e Glr	n Ala 20	Gln	Ser	Asn	Ala	Ile 25	Ser	Tyr	Ala	Gly	Cys 30	Ile	Ser		
G:	ln Me	t Tyı 35	Phe	Phe	Met	Val	Phe 40	Gly	Gly	lle	Asp	Thr 45	Phe	Leu	Leu		
T	nr Va 50		. Ala	Туг	Asp	Arg 55	Tyr	Val	Ala	ılle	: Суs 60	: His	Pro	Leu	Tyr		
T 6	yr Pr 5	o Va	l Ile	e Met	Asn 70	Pro	Arç	, Leu	Суя	Gly 75	Leu	ı Lev	ı Val	Leu	Val 80		
s	er Tr	p Ph	e Lev	ser 85	Leu	Ser	Туг	Ser	Leu 90	ı Ile	e Glr	n Ser	Leu	Leu 95	n Met		
L	eu Gl	n Le	u Sei 100		e Cys	Thr	s Sei	Trp 105	va:	l Il€	e Glr	n His	Phe 110	э Туі )	Cys		
G	lu L∈	eu Al 11		n Ala	Lev	Thi	Let 120	ı Ala	а Су	s Se	r Ası	o Thi 12!	r His	₃ Ile	e Asn		

<220>

<221> misc feature

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Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu Gly Phe Val Pro Phe
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Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val Ser Ser Ile Leu Arg
                    150
Ile Ser Ser Thr Asp Gly Lys His Lys Ala Phe Ser Asn Cys Gly Ser
His Leu Ser Val Val Phe Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
Leu Ser Ser Asn Ala Ser Ser Ser Trp Arg Gly Met Val Ala Ser
Val Met Tyr Thr Val Val Thr Pro
                        215
<210> 81
<211>
       647
<212> DNA
<213> Macaca sylvanus
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<223> Taxon = 9546; gene = MSY2; pseudogene; Accession DDBJ/EMBL/GenBank =
AF127869
<400> 81
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acagaacaaa gtcatcacct atgcaggctg catcagccag atgtgctttt tcatattctt
                                                                      120
tgcaggattg gacaccttta tgctgaccgt gatggcctac gacaggtttg tggccatctg
                                                                      180
tcaccctctg cactacacgg tcaccatgaa ccccaggetc tgtggactgc tggttctggc
                                                                      240
gtcctgatca tgagtgccct gaattcttca ttgcaaagct taatggtatt gcacctttcc
                                                                      300
ttctgtgcag acttggaaat tccccacttt ttctgtgaac ttaatcaggt catccacctt
                                                                      360
acctgttctg acacttttct taatgacatg gtgatgtatt tgtcagctgt gctgctgggt
                                                                      420
gggggatgtc tcattgggat cetttactet tactetaaga tegteteete tataettgea
                                                                      480
atctcatcag ttcaggggaa gtacaaggca ttttccacct gtgcatctca cctctcggtt
                                                                      540
gtctccttat ttattgtaca atcctaggtg tgtaccttag ttctgctgca acccacagct
                                                                      600
                                                                      647
cacacgcaag tgctgcagtc tcggtgatgt acactgtggt taccccc
<210> 82
 <211> 649
       DNA
 <212>
 <213> Macaca sylvanus
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<220 <221 <222 <223	.> C		(649 ict =	•	acto	ory n	ecep	otor									
	c at									ır Va	c co al Pr				et Va		49
aac Asn	atc Ile	cag Gln	aca Thr 20	cag Gln	agc Ser	aga Arg	gtc Val	atc Ile 25	acc Thr	tat Tyr	gca Ala	ggc Gly	tgc Cys 30	atc Ile	acc Thr		97
cag Gln	atg Met	tgc Cys 35	ttt Phe	ttc Phe	ata Ile	ttc Phe	ttt Phe 40	gtg Val	gga Gly	ctg Leu	gat Asp	atc Ile 45	ttt Phe	atg Met	ctg Leu		145
acc Thr	gtg Val 50	atg Met	gcc Ala	ttt Phe	gac Asp	cgg Arg 55	ttt Phe	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	cac His		193
tac Tyr 65	acg Thr	gtc Val	acc Thr	atg Met	aac Asn 70	ccc Pro	agg Arg	ctc Leu	agt Ser	999 Gly 75	ctg Leu	ctg Leu	gtt Val	ctg Leu	gcg Ala 80		241
tcc Ser	tgg Trp	atc Ile	atg Met	agt Ser 85	gcc Ala	ctg Leu	aat Asn	tcc Ser	tcg Ser 90	tta Leu	caa Gln	agc Ser	tta Leu	ata Ile 95	gtg Val		289
ctg Leu	cgg Arg	ctt Leu	tcc Ser 100	ttc Phe	tgc Cys	aca Thr	gac Asp	ttg Leu 105	gaa Glu	att Ile	ccc Pro	cac His	ttt Phe 110	ttc Phe	tgt Cys		337
gaa Glu	ctt Leu	aat Asn 115	cag Gln	gtg Val	gtc Val	cac His	ctt Leu 120	gcc Ala	tgt Cys	tct Ser	gac Asp	acc Thr 125	ttt Phe	ctt Leu	aat Asn		385
gac Asp	atg Met 130	gtg Val	atg Met	tat Tyr	ttg Leu	gca Ala 135	tct Ser	gca Ala	ctg Leu	ctg Leu	ggc Gly 140	tgt Cys	ggt Gly	ccc Pro	ctc Leu		433
tct Ser 145	Gly aaa	atc Ile	ctt Leu	tat Tyr	tct Ser 150	tat Tyr	tct Ser	aag Lys	atc Ile	gtt Val 155	tcc Ser	tcc Ser	ata Ile	cgt Arg	gga Gly 160		481
atc Ile	tca Ser	tca Ser	gct Ala	cag Gln 165	gjå aaa	aag Lys	tac Tyr	agg Arg	gca Ala 170	ttt Phe	tcc Ser	acc Thr	tgt Cys	gca Ala 175	tct Ser		529
cac His	ctc Leu	tca Ser	gtt Val 180	gtc Val	tcc Ser	tta Leu	ttt Phe	tat Tyr 185	ggt Gly	acg Thr	ctc Leu	cta Leu	gga Gly 190	gtg Val	tac Tyr		577
ttt Phe	agt Ser	tct Ser 195	gct Ala	gca Ala	acc Thr	cgt Arg	aac Asn 200	Ser	cac His	tca Ser	agt Ser	gct Ala 205	Ala	gcc Ala	tcg Ser		625
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Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala Gly Cys Ile Thr 20 25 30

Gln Met Cys Phe Phe Ile Phe Phe Val Gly Leu Asp Ile Phe Met Leu 35 40 45

Thr Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Thr Val Thr Met Asn Pro Arg Leu Ser Gly Leu Leu Val Leu Ala 65 70 75 80

Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Ile Val

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys 100 105 110

Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125

Asp Met Val Met Tyr Leu Ala Ser Ala Leu Leu Gly Cys Gly Pro Leu 130 135 140

Ser Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Gly 145 150 155

Ile Ser Ser Ala Gln Gly Lys Tyr Arg Ala Phe Ser Thr Cys Ala Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 180 185 190

Phe Ser Ser Ala Ala Thr Arg Asn Ser His Ser Ser Ala Ala Ala Ser 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

<210 <211 <212 <213	> 6 > D	4 46 NA acac	a sy	lvan	us											
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aac Asn	ctc Leu	cag Gln	tcc Ser 20	cag Gln	aac Asn	aaa Lys	gcc Ala	atc Ile 25	tcc Ser	tat Tyr	gca Ala	Gly aaa	tgt Cys 30	ctg Leu	aca Thr	97
cag Gln	ctc Leu	tac Tyr 35	ttc Phe	ctg Leu	gtc Val	tcc Ser	ttg Leu 40	gtg Val	gcc Ala	ctg Leu	gac Asp	aac Asn 45	ctc Leu	atc Ile	ctg Leu	145
gct Ala	gtg Val 50	atg Met	gcg Ala	tat Tyr	gac Asp	cgc Arg 55	tat Tyr	gtg Val	gcc Ala	atc Ile	tgc Cys 60	tgc Cys	ccc Pro	ctc Leu	cac His	193
tac Tyr 65	acc Thr	aca Thr	gcc Ala	atg Met	agc Ser 70	cct Pro	aag Lys	ctc Leu	tgt Cys	atc Ile 75	tta Leu	ctc Leu	ctt Leu	tcc Ser	ttg Leu 80	241
tgt Cys	tgg Trp	gtc Val	tta Leu	tct Ser 85	gtg Val	ctc Leu	tat Tyr	ggc Gly	ctc Leu 90	ata Ile	cac His	acc Thr	ttc Phe	ctc Leu 95	atg Met	289
acc Thr	acg Thr	gtg Val	acc Thr 100	ttc Phe	tgt Cys	gly ggg	tca Ser	cga Arg 105	aaa Lys	atc Ile	cac His	tac Tyr	atc Ile 110	ttc Phe	tgt Cys	337
gag Glu	atg Met	tat Tyr 115	Val	ttg Leu	ctg Leu	agg Arg	ctg Leu 120	Ата	tgt Cys	tcc Ser	gac Asp	act Thr 125	cag Gln	att Ile	aat Asn	385
cac His	aca Thr 130	Val	ctg Leu	att Ile	gcc Ala	aca Thr 135	ggc Gly	tgc Cys	ttt Phe	atc Ile	ttc Phe 140	ctc Leu	att Ile	ccc Pro	ttt Phe	433
gga Gly 145	ttc Phe	atg Met	atc Ile	att Ile	tcc Ser 150	Tyr	gtg Val	ttg Leu	att Ile	gtc Val 155	aga Arg	gcc Ala	atc Ile	ctc Leu	aga Arg 160	481
ata Ile	ccc	tca Ser	gtc Val	tct Ser 165	Lys	aaa Lys	tac Tyr	aaa Lys	gcc Ala 170	Phe	tcc Ser	act Thr	tgt Cys	gcc Ala 175	tcc Ser	529
cat His	ttg Leu	ggt Gly	gta Val 180	Val	tcc Ser	ctc Leu	ttc Phe	tat Tyr 185	Gly	aca Thr	ctt Leu	cgt Arg	atg Met 190	vaı	tac Tyr	577
ctg	aaç	g ccc	ctc	cat	acc	tac	tct	gtg	aag 73		: tca	gta	gcc	aca	gtg	625

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                                                                      646
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Met Tyr Ala Val Val Thr Pro
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<223> Taxon = 9546; gene = MSY6; Accession DDBJ/EMBL/GenBank = AF127871
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Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Ile Leu
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu His
Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu Ser Leu
65
Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr Phe Leu Met
Thr Thr Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr Ile Phe Cys
                                 105
            100
Glu Met Tyr Val Leu Leu Arg Leu Ala Cys Ser Asp Thr Gln Ile Asn
                             120
His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu Ile Pro Phe
Gly Phe Met Ile Ile Ser Tyr Val Leu Ile Val Arg Ala Ile Leu Arg
145
Ile Pro Ser Val Ser Lys Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Arg Met Val Tyr
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## Leu Lys Pro Leu His Thr Tyr Ser Val Lys Asp.Ser Val Ala Thr Val 195 200 205

Met Tyr Ala Val Val Thr Pro 210 215

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aac at Asn Il															97
cag gt Gln Va															145
acc gt Thr Va 50	g atg l Met	gct Ala	tat Tyr	gac Asp	cgg Arg 55	ttt Phe	gtg Val	gcc Ala	gtc Val	tgc Cys 60	cac His	ccc Pro	ctg Leu	cac His	193
tat gt Tyr Va 65															241
acg tg Thr Tr															289
acg ca Thr Hi															337
gaa ct Glu Le		His	Ile		Gln	Leu	Ala	Cys		Asp	Thr	Phe			385
agc ac Ser Th 13	r Leu	ata Ile	tat Tyr	gtt Val	atg Met 135	aca Thr	ggt Gly	gtg Val	ctg Leu	ggc Gly 140	gtt Val	ttt Phe	ccc Pro	ctc Leu	433
ctt gg Leu Gl 145															481
atg tc	c tca	tct	ggg	gga	aaa	gag	aaa	gca	ctt	tct	acc	tgt	ggc	tct	529

Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser 165 170 175
cac ctc tcc atc gtt tct tta ttt tat ggg aca ggc att ggg gtc cat His Leu Ser Ile Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His 180 185 190
ttc act tct gcg gtg act cat tct tcc cag aac atc tcc gtg gcc tcg Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser 195 200 205
gtg atg tac acg gtg gtt acc ccc 649 Val Met Tyr Thr Val Val Thr Pro 210 215
<210> 87 <211> 216 <212> PRT <213> Macaca sylvanus
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Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr 20 25 30
Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu 35 40 45
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His 50 55 60
Tyr Val Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val 65 70 75 80
Thr Trp Leu Ile Gly Val Met Thr Pro Leu Leu His Ile Ser Leu Leu 85 90 95
Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys 100 105 110
Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125
Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu 130 135 140
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<221> CDS <222> (2)

(2)..(649)

<223> Product = olfactory receptor

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Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
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                            200
Val Met Tyr Thr Val Val Thr Pro
<210> 88
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AF127873
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tgctggaatg gatactttcc tactggccat gatggcctat gaccggtttg tggccatctg
                                                                     180
ccacccctg cactacacgg tcatcatgaa cccctgcctc tgtggcatcc tggttctggc
                                                                     240
                                                                     300
atcttgattc atcattttat gggtctccct agttcatatt ctactgatga agagtttgat
                                                                     360
ctccataggc actgagattc cgcatttctt ctgtgaactg gctcaggtcc tcaaggtgcc
cyctctqata ctctcctcgt taacattgtc ttgtatgtgg ccacagcact gctgggtgtg
                                                                     420
cttcctgtag ctgggatcct cttctcctac tctcagatcg tctcctcctt aatgaggatg
                                                                     480
tcctccaccg agggcaagta caaagccttt tccacctgtg ggtctcacct ctgtgtggtc
                                                                     540
tccttgttct atggaacagg acttggggtc tatctcagtt ctgctgtgac ccattcttcc
                                                                     600
                                                                     645
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cag atg ta Gln Met Ty 35	r Phe Phe										145
acc gtg at Thr Val Me 50	g gcc tat t Ala Tyr	gac cgg Asp Arg 55	tat gto	g gcc . Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	tac Tyr	193
tac cct gt Tyr Pro Va 65	c att atg l Ile Met	aac ccc Asn Pro 70	cgc cto Arg Lev	tgt Cys	ggc Gly 75	ctg Leu	ctg Leu	gtt Val	ctt Leu	gtg Val 80	241
tcc tgg tt Ser Trp Ph	c ctc agc le Leu Ser 85	ttg tca Leu Ser	tac tcc Tyr Sei	ctg Leu 90	atc Ile	cag Gln	agt Ser	ctg Leu	ttg Leu 95	atg Met	289
ctg cag tt Leu Gln Le	g tcc ttt u Ser Phe 100	tgc acc Cys Thr	agt tgg Ser Trp 109	Val	att Ile	cag Gln	cac His	ttt Phe 110	tac Tyr	tgc Cys	337
gag ctt gc Glu Leu Al 11	a Gln Ala	ctc acg Leu Thr	ctt gcc Leu Ala 120	tgc Cys	tca Ser	gac Asp	aca Thr 125	cac His	atc Ile	aat Asn	385
tac atc ct Tyr Ile Le 130	g ctc tac eu Leu Tyr	gtg gtg Val Val 135	acc ggo Thr Gly	ctt Leu	ctg Leu	ggt Gly 140	ttt Phe	gtg Val	ccc Pro	ttc Phe	433
tca gga at Ser Gly Il 145	c ctt ttc e Leu Phe	tcc tac Ser Tyr 150	acc caa Thr Gli	a att 1 Ile	gtc Val 155	tcc Ser	tcc Ser	atc Ile	ctg Leu	aga Arg 160	481
atc tca tc Ile Ser Se	c aca gat r Thr Asp 165	ggg aaa Gly Lys	cac aaa His Lys	gcc Ala 170	ttt Phe	tct Ser	acc Thr	tgc Cys	gga Gly 175	tct Ser	529
cat ctg to His Leu Se				Gly							577
ctt agt to Leu Ser Se 19	er Asn Ala	tcg tcc Ser Ser	tct tcc Ser Ser 200	tgg Trp	cgg Arg	ggc Gly	atg Met 205	gtg Val	gcc Ala	tcg Ser	625
gtc atg ta Val Met Ty 210											649
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Gln Met Tyr Phe Phe Met Val Phe Gly Gly Ile Asp Thr Phe Leu Leu

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr

Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val

Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met

Leu Gln Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys

Glu Leu Ala Gln Ala Leu Thr Leu Ala Cys Ser Asp Thr His Ile Asn

Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu Gly Phe Val Pro Phe

Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val Ser Ser Ile Leu Arg

Ile Ser Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr Cys Gly Ser 165

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Leu Ser Ser Asn Ala Ser Ser Ser Trp Arg Gly Met Val Ala Ser 195 200

Val Met Tyr Thr Val Val Thr Pro

<210> 91

<211> 649 <212> DNA

<213> Callithrix jacchus

<220>

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aac Asn	atc Ile	cag Gln	aca Thr 20	cac His	agc Ser	aaa Lys	gtc Val	atc Ile 25	acc Thr	tat Tyr	gca Ala	ggc Gly	tgc Cys 30	gtc Val	acc Thr	97
cag Gln	ttg Leu	tac Tyr 35	ttc Phe	ttt Phe	gta Val	ctc Leu	ttc Phe 40	ata Ile	Gly 999	t <b>t</b> g Leu	gac Asp	agc Ser 45	tta Leu	ctc Leu	ccg Pro	145
acc Thr	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgg Arg 55	ttt Phe	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	cac His	193
tac Tyr 65	acg Thr	gtc Val	atc Ile	atg Met	aac Asn 70	cct Pro	cag Gln	ttc Phe	tgt Cys	gga Gly 75	ctg Leu	ctg Leu	gtt Val	ctg Leu	gtg Val 80	241
tcc Ser	tgg Trp	atc Ile	atg Met	agt Ser 85	gcc Ala	ctg Leu	cat His	tct Ser	ttg Leu 90	aca Thr	gaa Glu	agc Ser	tta Leu	atg Met 95	gta Val	289
tac Tyr	cca Pro	ctg Leu	ctc Leu 100	ttt Phe	tgt Cys	aca Thr	gac Asp	ttg Leu 105	aaa Lys	atc Ile	ccc Pro	cag Gln	ttt Phe 110	ttc Phe	tgt Cys	337
gaa Glu	att Ile	cat His 115	cag Gln	ata Ile	att Ile	caa Gln	ttt Phe 120	gcc Ala	tgt Cys	tct Ser	gac Asp	acc Thr 125	ttt Phe	ctt Leu	aat Asn	385
aac Asn	ctg Leu 130	gtg Val	atg Met	tat Tyr	ttg Leu	tca Ser 135	act Thr	gtg Val	ctc Leu	ctg Leu	ggc Gly 140	ggt Gly	ggt Gly	ccc Pro	ctt Leu	433
gct Ala 145	G1 y 999	atc Ile	ctg Leu	tac Tyr	tct Ser 150	tac Tyr	tct Ser	aag Lys	ata Ile	gct Ala 155	tcc Ser	tct Ser	ata Ile	cgt Arg	gca Ala 160	481
atc Ile	tca Ser	tca Ser	gct Ala	gag Glu 165	999 999	aag Lys	tac Tyr	aag Lys	gca Ala 170	ttt Phe	tcc Ser	acc Thr	tgt Cys	gca Ala 175	tct Ser	529
cac His	ctc Leu	tca Ser	gtt Val 180	gtc Val	tcc Ser	tta Leu	ttt Phe	tat Tyr 185	tgt Cys	aca Thr	ggc Gly	cta Leu	999 Gly 190	gtg Val	tac Tyr	577
ctg Leu	agt Ser	tct Ser 195	gct Ala	gca Ala	acc Thr	cac His	agc Ser 200	tca Ser	ctc Leu	tca Ser	agc Ser	gca Ala 205	gca Ala	gcc Ala	tcg Ser	625
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<213> Callithrix jacchus

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Gln Leu Tyr Phe Phe Val Leu Phe Ile Gly Leu Asp Ser Leu Leu Pro 35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Thr Val Ile Met Asn Pro Gln Phe Cys Gly Leu Leu Val Leu Val 65 70 75 80

Ser Trp Ile Met Ser Ala Leu His Ser Leu Thr Glu Ser Leu Met Val 85 90 95

Tyr Pro Leu Leu Phe Cys Thr Asp Leu Lys Ile Pro Gln Phe Phe Cys 100 105 110

Glu Ile His Gln Ile Ile Gln Phe Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125

Asn Leu Val Met Tyr Leu Ser Thr Val Leu Leu Gly Gly Pro Leu 130 135 140

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Ala Ser Ser Ile Arg Ala 145 150 155 160

Ile Ser Ser Ala Glu Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Leu Gly Val Tyr 180 185 190

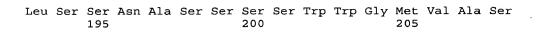
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Val Met Tyr Thr Val Val Thr Pro 210 215

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aac atc cag gag cag agt ggt acc atc agc tat gca ggc tgc att gcc
                                                                       97
Asn Ile Gln Glu Gln Ser Gly Thr Ile Ser Tyr Ala Gly Cys Ile Ala
                                                                      145
cag atg tat ttt ttc atg gtt ttt gga ggc atg gac aca ttt ctc ctc
Gln Met Tyr Phe Phe Met Val Phe Gly Gly Met Asp Thr Phe Leu Leu
                            40
                                                                      193
act gtg atg gcc tat gac cgg tat gtg gct atc tgt cac ccc ctg tcc
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Ser
tac cct gtc att gta aac ccc cgc ctc tgc ggc ctg ttg gtt ctt gtg
                                                                      241
Tyr Pro Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val
                    70
65
                                                                      289
tcc tgg ttc ctc agc ttg tca tac tcc ctg atc cag agt ctg ttg atg
Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
                                                                      337
ctg cgg cta tcc ttc tgc acc agt tgg gtc att cag cac ttt tac tgt
Leu Arg Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys
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                                                                      385
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Glu Leu Ala Gln Val Leu Thr Leu Ala Cys Ser Asp Thr His Val Asn
                            120
                                                125
                                                                      433
tac atc ctg ctc tac atg gtg acc ggc ctt ctg ggc tgt gtt ccc ttc
Tyr Ile Leu Leu Tyr Met Val Thr Gly Leu Leu Gly Cys Val Pro Phe
tca ggg atc ctt ttc tcc tac atc caa att gtc tcc tcc atc ctg aga
                                                                      481
Ser Gly Ile Leu Phe Ser Tyr Ile Gln Ile Val Ser Ser Ile Leu Arg
145
                    150
                                                             160
atc cca tcc aca gat ggg aaa cat aaa gcc ttt tct acc tgt gga tct
                                                                      529
Ile Pro Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr Cys Gly Ser
cat ctg tct gtg gtt tct tta ttc tac ggg aca ggc ctt ggt gtc tac
                                                                      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
            180
                                185
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ctt agc tcc aat gcc tcg tcc tct tcc tgg tgg ggc atg gtg gcc tca Leu Ser Ser Asn Ala Ser Ser Ser Trp Trp Gly Met Val Ala Ser 195 200 205	25
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Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Ser 50 55 60	
Tyr Pro Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val 65 70 75 80	
Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met 85 90 95	
Leu Arg Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys 100 105 110	
Glu Leu Ala Gln Val Leu Thr Leu Ala Cys Ser Asp Thr His Val Asn 115 120 125	
Tyr Ile Leu Leu Tyr Met Val Thr Gly Leu Leu Gly Cys Val Pro Phe 130 135 140	
Ser Gly Ile Leu Phe Ser Tyr Ile Gln Ile Val Ser Ser Ile Leu Arg 145 150 155 160	
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His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr 180 185 190	



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aat Asn	ttt Phe	cta Leu	tca Ser 20	G1 y 999	aca Thr	aag Lys	gtt Val	atc Ile 25	ccc Pro	tac Tyr	atg Met	ggc Gly	tgc Cys 30	ctg Leu	gtc Val	97
		tac Tyr 35														145
		atg Met														193
		gtg Val														241
		agc Ser														289
		ctg Leu														337
gac Asp	acc Thr	cag Gln 115	cct Pro	gtg Val	cta Leu	aag Lys	ctg Leu 120	tcc Ser	tgc Cys	tct Ser	gac Asp	acg Thr 125	tcc Ser	tcc Ser	agc Ser	385
_	_	gtg Val	_	_					_	_						433
		atc Ile														481

atc ccc ttt gca gct ggg aag tgg agg gcc ttc tct acc tgt ggc Ile Pro Phe Ala Ala Gly Lys Trp Arg Ala Phe Ser Thr Cys Gly 165 170 175	/ Ser												
cac ctc act gta gta gcc ctt ttc tac ggg agt ata tat tat gtc His Leu Thr Val Val Ala Leu Phe Tyr Gly Ser Ile Tyr Tyr Val 180 185 190	tat 577 Tyr												
ttt agg ccc ctg tcc atg tac tca gtg gtg aag gac cga gta gcc Phe Arg Pro Leu Ser Met Tyr Ser Val Val Lys Asp Arg Val Ala 195 200 205	c aca 625 a Thr												
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Tyr Asp Val Ala Met Asn Pro Arg His Cys Leu Leu Met Leu Leu 65 70 75	ı Gly 80												
Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu 85 90 95	ı Met												
Ser His Leu Ser Phe Cys Ala Ser His Val Ile Lys His Phe Phe 100 105 110	e Cys												
Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser 115 120 125	s Ser												
Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro 130 135 140	o Phe												
Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu 145 150 155	ı Arg 160												

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Ile Pro Phe Ala Ala Gly Lys Trp Arg Ala Phe Ser Thr Cys Gly Ser
                165 170
His Leu Thr Val Val Ala Leu Phe Tyr Gly Ser Ile Tyr Tyr Val Tyr
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Phe Arg Pro Leu Ser Met Tyr Ser Val Val Lys Asp Arg Val Ala Thr
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Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
            20
                                 25
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Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu
act gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac cca ctg cac
                                                                         193
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
                         55
                                                                         241
tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca
Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
tee tgg ate etg agt gee etg aat tee tea tta caa ace tta ata gtg
                                                                         289
Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val
                                      90
                85
ctg cgg ctt tcc ttc tgc aca gac ttg gaa atc ccc cac ttt ttc tgc
                                                                         337
Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
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gca ggg att ctt tac tct tac tct aag ata gtt tcc tcc ata cgt gca Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 145 150 155 160	481
atc tca tca gct cag ggg aag tac aag gca ttt tcc acc tgt gta tct Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser 165 170 175	529
cac atc tta att gtc tcc tta ttt tat ggt aca ctc cta ggt gtg tac His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 180 185 190	577
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	XF 1 Z / O / O
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Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val 1 15  Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr 20  Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu 40  Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His	AT 12 / 0 / 0
Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val 15  Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr 20  Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu 40  Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His 50  Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala	AT 12 / 0 / 0
Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val 1 10    Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr 20    Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu 45    Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His 50    Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala 80    Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val	AT 12/0/0

130 135 140
Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 145 150 155 160
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser 165 170 175
His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 180 185 190
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Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys 100 105 110	7
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aaa atc gtg atg tat ttt gtg aca att gca atg ggt gtt ttt cct ctc Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu 130 135 140	3
tct gga atc cta tac tct tat tct cag att ttc tcc tcc atc ctg aga  Ser Gly Ile Leu Tyr Ser Tyr Ser Gln Ile Phe Ser Ser Ile Leu Arg  145 150 155 160	1
gta tca cct gcc caa ggc cag cac aaa gcc ttt tcc acc tgt ggg tct Val Ser Pro Ala Gln Gly Gln His Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175	9
cac ctc tca gtg gtc acc ctg ttc tat ggc acg ggc ctt ggg gta tat 57 His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr 180 185 190	7
ctc agt ctt gca gct aca cca tct tct agg aca agt ctg atg gcc tcg Leu Ser Leu Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Met Ala Ser 195 200 205	5
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Lys	Ile 130	Val	Met	Tyr	Phe	Val 135	Thr	Ile	Ala	Met	Gly 140	Val	Phe	Pro	Leu	
Ser 145	Gly	Ile	Leu	Tyr	Ser 150	Tyr	Ser	Gln	Ile	Phe 155	Ser	Ser	Ile	Leu	Arg 160	
Val	Ser	Pro	Ala	Gln 165	Gly	Gln	His	Lys	Ala 170	Phe	Ser	Thr	Cys	Gly 175	Ser	
His	Leu	Ser	Val 180	Val	Thr	Leu	Phe	Tyr 185	Gly	Thr	Gly	Leu	Gly 190	Val	Tyr	
Leu	Ser	Leu 195	Ala	Ala	Thr	Pro	Ser 200	Ser	Arg	Thr	Ser	Leu 205	Met	Ala	Ser	
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		caa Gln														97
cag Gln	atg Met	tct Ser 35	ttt Phe	tca Ser	atc Ile	ttt Phe	ttt Phe 40	gtg Val	tgt Cys	atg Met	gaa Glu	gac Asp 45	atg Met	ctc Leu	ctt Leu	145
gct Ala	gtg Val	atg Met	gcc Ala	tat Tyr	gac Asp	cgg Arg	ttt Phe	gtg Val	gcc Ala	atc Ile	tgt Cys	cac His	cct Pro	ctg Leu	cac His	193

			ggc ttc tta gtg Gly Phe Leu Val 75												
			gtg cac aat ttg Val His Asn Leu												
Leu Gln Phe S			att tct aat ttc Ile Ser Asn Phe 110												
			tcc gac acg ttt Ser Asp Thr Phe 125												
			gta ttt ggt ttt Val Phe Gly Phe 140												
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			gcc ttc tct acc Ala Phe Ser Thr												
Ser His Leu A			gga aca gtc ctt Gly Thr Val Leu 190												
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Ala Val Met A	la Tyr Asp Arg 55	Phe Val Ala	Ile Cys His Pro 60	Leu His											

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Ser Ala Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val
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                                105
Asp Pro Ser Gln Leu Leu Thr Leu Ala Cys Ser Asp Thr Phe Val Asn
Asn Asn Ile Val Met Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro
Ile Ser Gly Ile Phe Leu Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu
Arg Val Pro Ser Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser
                                    170
Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Leu Gly Val
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Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr

25

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tac Tyr 65	aca Thr	gtc Val	acc Thr	att Ile	aac Asn 70	ccc Pro	aga Arg	ctg Leu	tgt Cys	gga Gly 75	ctg Leu	ctg Leu	gtt Val	ctg Leu	gca Ala 80	241
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gca Ala 145	gly aaa	att Ile	ctt Leu	tac Tyr	tct Ser 150	tac Tyr	tct Ser	aag Lys	ata Ile	gtt Val 155	tcc Ser	tcc Ser	ata Ile	cgt Arg	gca Ala 160	481
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cac His	atc Ile	tta Leu	att Ile 180	gtc Val	tcc Ser	tta Leu	Phe	tat Tyr 185	ggt Gly	aca Thr	ctc Leu	cta Leu	ggt Gly 190	gtg Val	tac Tyr	577
ctt Leu	agt Ser	tct Ser 195	gct Ala	gca Ala	act Thr	Gly .	aac Asn 200	tca Ser	cat His	tca Ser	Arg	gct Ala 205	gca Ala	gcc Ala	tcg Ser	625
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Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His 55 60

Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala

Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys

Val Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn 120

Asp Val Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Pro Leu 130

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 145 150

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser 170 165

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gcc tct atg gcc atc gac cgg ctg gtg gcc atc tgc aac ccc tta cac Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His 50 55 60	193
tat gat gtg gct atg aac tcc cgg cgt tgc cta ctc atg cta ttg ggt Tyr Asp Val Ala Met Asn Ser Arg Arg Cys Leu Leu Met Leu Leu Gly 65 70 75 80	241
tct tgc agc atc tcc cac cta cat tcc ctg ttc cgg gtg cta ctt atg Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met 85 90 95	289
tct cgc ctg tct ttc tgt gcc tcc cac gtc att aag cac ttt ttc tgt Ser Arg Leu Ser Phe Cys Ala Ser His Val Ile Lys His Phe Phe Cys 100 105 110	337
gac acc cag cct gtg cta aag ctg tcc tgc tct gac acg tcc tcc agc Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser 115 120 125	385
cag atg gtg gtc atg act gag acc tta gct gtt att gtg acc ccc ttc Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe 130 135 140	433
ctg tgt atc atc ttc tcc tac ctg cga atc atc act gtg ctc aga Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Arg 145 150 155 160	481
atc ccc tct gca gcc ggg aag tgg agg gcc ttc tct acc tgt ggc tcc Ile Pro Ser Ala Ala Gly Lys Trp Arg Ala Phe Ser Thr Cys Gly Ser 165 170 175	529
cac ctc act gta gta gcc ctt ttc tac ggg agt att att tat gtc tat His Leu Thr Val Val Ala Leu Phe Tyr Gly Ser Ile Ile Tyr Val Tyr 180 185 190	577
ttt agg ccc ctg tcc atg tac tca gtg gtg aag gac cga gta gcc aca Phe Arg Pro Leu Ser Met Tyr Ser Val Val Lys Asp Arg Val Ala Thr 195 200 205	625
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Pro Met Tyr Phe Phe Met Ala Phe Ala Asn Thr Asp Ser Tyr Leu Leu 35 40 45

Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His 50 55 60

Tyr Asp Val Ala Met Asn Ser Arg Arg Cys Leu Leu Met Leu Leu Gly 65 70 75 80

Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met 85 90 95

Ser Arg Leu Ser Phe Cys Ala Ser His Val Ile Lys His Phe Cys 100 105 110

Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser 115 120 125

Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe 130 140

Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Arg 145 150 155 160

Ile Pro Ser Ala Ala Gly Lys Trp Arg Ala Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Thr Val Val Ala Leu Phe Tyr Gly Ser Ile Ile Tyr Val Tyr \$180\$

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<211> 649

<212> DNA

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cag Gln	att Ile	ttt Phe 35	ttt Phe	ttc Phe	gtt Val	gca Ala	ttt Phe 40	gga Gly	tgc Cys	ctg Leu	gac	aat Asn 45	ttg Leu	ctc	ttg Leu	145
acc Thr	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgg Arg 55	ttc Phe	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac	ccc Pro	ctg Leu	cac His	193
tac Tyr 65	gcg Ala	gtc Val	atc Ile	atg Met	aac Asn 70	ccc Pro	cgg Arg	ctc Leu	tgt Cys	aga Arg 75	ctg Leu	cta Leu	gtt Val	ctg Leu	80 Gly 333	241
tcc Ser	tgg Trp	tgc Cys	atc Ile	agt Ser 85	gtc Val	atg Met	gtt Val	tct Ser	ctg Leu 90	ctc Leu	gag Glu	acc Thr	ttg Leu	acc Thr 95	att Ile	289
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gat Asp	gtt Val	ctc Leu 115	gaa Glu	gtc Val	ctg Leu	aag Lys	ctc Leu 120	gcc Ala	tgt Cys	tct Ser	gaa Glu	acc Thr 125	ctc Leu	gtc Val	aat Asn	385
aaa Lys	atc Ile 130	gtg Val	atg Met	tat Tyr	ttt Phe	gtg Val 135	aca Thr	att Ile	gca Ala	atg Met	ggt Gly 140	gtt Val	ttt Phe	cct Pro	ctc Leu	433
tct Ser 145	gga Gly	atc Ile	cta Leu	tac Tyr	tct Ser 150	tat Tyr	tct Ser	cag Gln	att Ile	ttc Phe 155	tcc Ser	tcc Ser	atc Ile	ctg Leu	aga Arg 160	481
gta Val	tca Ser	cct Pro	gcc Ala	caa Gln 165	ggc Gly	cag Gln	cac His	aaa Lys	gcc Ala 170	ttt Phe	tcc Ser	acc Thr	tgt Cys	999 Gly 175	tct Ser	529
cac His	ctc Leu	tca Ser	gtg Val 180	gtc Val	acc Thr	ctg Leu	ttc Phe	tat Tyr 185	ggc Gly	acg Thr	ggc Gly	ctt Leu	999 Gly 190	gta Val	tat Tyr	577
ctc Leu	agt Ser	tct Ser 195	gca Ala	gct Ala	aca Thr	cca Pro	tct Ser 200	tct Ser	agg Arg	aca Thr	agt Ser	ctg Leu 205	atg Met	gcc Ala	tcg Ser	625
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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His

Tyr Ala Val Ile Met Asn Pro Arg Leu Cys Arg Leu Leu Val Leu Gly

Ser Trp Cys Ile Ser Val Met Val Ser Leu Leu Glu Thr Leu Thr Ile

Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Cys 105

Asp Val Leu Glu Val Leu Lys Leu Ala Cys Ser Glu Thr Leu Val Asn 120

Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu 135

Ser Gly Ile Leu Tyr Ser Tyr Ser Gln Ile Phe Ser Ser Ile Leu Arg 150

Val Ser Pro Ala Gln Gly Gln His Lys Ala Phe Ser Thr Cys Gly Ser

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Val Met Tyr Thr Met Val Thr Pro 210 215

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													tgc Cys 30			9	7
													ttg Leu			14	5
													ccc Pro			19	3
													gtt Val			24	1
													ttg Leu			28	9
_		_			_			_	_				ttt Phe 110		-	33	7
													ctc Leu			38	5
													ttt Phe			43	3
													atc Ile			48	1
													tgt Cys			52	9
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Gln Ile Phe Phe Phe Val Ala Phe Gly Cys Leu Asp Asn Leu Leu Leu

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His

Tyr Ala Val Ile Met Asn Pro Arg Leu Cys Arg Leu Leu Val Leu Gly

Ser Trp Cys Ile Ser Val Met Val Ser Leu Leu Glu Thr Leu Thr Ile 90 85

Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Cys 100 105 110

Asp Val Leu Glu Val Leu Lys Leu Ala Cys Ser Glu Thr Leu Val Asn 115 120 125

Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu

Ser Gly Ile Leu Tyr Ser Tyr Ser Gln Ile Phe Ser Ser Ile Leu Arg

Val Ser Pro Ala Gln Gly Gln His Lys Ala Phe Ser Thr Cys Gly Ser

His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr 180 185

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tggaggcgtg gaagagagac atgctcctga gtgtgaaggc ctatgaccgg tttgtagcca
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cctgtcaccc tctgtatcat tcagccatca tgaagtcatg tttctgtggc tttctagttt
                                                                         240
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ccccatcttg catgttgtga cagcttcacc gataacatca tcacgtatct ccctgacgcc
                                                                         420
atatececet ttatteceat eteggggace etttteteta taatateaaa ttgttteete
                                                                         480
cattetgagg getteateat caggtgggag gtataaagee ttetecatet gtgggtetea
                                                                         540
cctgtcagtt gtttgcttat tttatggaac aggcatatgg gggtacctca gttcagatgt
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  1
                   5
                                        10
gac atg caa act cac age aga gtc atc tcc tat gca ggc tgc ctg act
                                                                          97
Asp Met Gln Thr His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
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Leu Ser Ser Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Met Ala Ser

195

cag atg t Gln Met S	cct ttt Ser Phe 35	ttt gtc Phe Val	Leu	ttt Phe 40	gca Ala	tgt Cys	atg Met	gat Asp	gac Asp 45	atg Met	ctt Leu	ctg Leu	145	5
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tac cca g Tyr Pro V 65	gtt acc /al Thr	atg aac Met Asn 70	cca Pro	tgt Cys	ttc Phe	tg <b>t</b> Cys	ggc Gly 75	ttc Phe	cta Leu	gtt Val	ttg Leu	ttg Leu 80	24	1
tct ttt t Ser Phe F													289	Э
tta caa a Leu Gln I													33'	7
gac cct t Asp Pro S			His										385	5
gac ata g Asp Ile V 130													433	3
ttg ggg a Leu Gly I 145													48	1
gtt tca t Val Ser S													529	Э
cac ctg t His Leu S													57	7
ctc agt t Leu Ser S 1			Ser '										625	5
gtg atg t Val Met T 210													649	€
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Gln Met Ser Phe Phe Val Leu Phe Ala Cys Met Asp Asp Met Leu Leu

Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Pro Asp

Tyr Pro Val Thr Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu Leu

Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Trp Ile Ala 85 90

Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Cys 100 105

Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Asn

Asp Ile Val Met Tyr Phe Leu Ala Ala Ile Phe Gly Phe Leu Pro Ile

Leu Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu Arg

Val Ser Ser Ser Gly Gly Arg Tyr Lys Ala Phe Ala Thr Cys Gly Ser 165

His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr Ala Leu Gly Gly Tyr

Leu Ser Ser Asp Met Ser Ser Tyr Pro Arg Lys Gly Ala Val Ala Ser

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ggcacggaag agagacatgc teetgagtgt gatggeetat gaccggtttg tagecatetg
                                                                        180
 tcaccctcta tatcattcag tcatcatgag cccgtgtttc tgtggcttcc tagttttgtt
                                                                        240
 gtcttttttt ttcttctcag tcttttagac tcccagctgc accacttgat tgccttgcta
                                                                        300
 atgacctact tcaaggatgt ggaaattccg aatttcttct gtgatccttc tcaactcccc
                                                                       360
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 tttgcttttc ttcccatctc ggggactctt ttctcttact ctaatattgt ctcctccatt
                                                                       480
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                                       10
aac atc cag gca cgg agc aaa gaa atc tcc tac atg ggg tgc ctc act
                                                                        97
Asn Ile Gln Ala Arg Ser Lys Glu Ile Ser Tyr Met Gly Cys Leu Thr
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cag gtg tat ttt tta atg atg ttt gct gga atg gat act ttc cta ctg
                                                                       145
Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr Phe Leu Leu
                            40
gct gtg atg gct tat gac cgg ttt gtg gcc atc tgc cac ccc ctt cag
                                                                       193
Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Gln
    5.0
                        55
tac gcg gtc atc atg aac ccc cat ctc tgt ggc ctg ctg gtt ctg gca
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Tyr Ala Val Ile Met Asn Pro His Leu Cys Gly Leu Leu Val Leu Ala
                    70
tet tgg tte ate att tte tgg gte tee etg gtt cat att eta etg atg
                                                                      289
Ser Trp Phe Ile Ile Phe Trp Val Ser Leu Val His Ile Leu Leu Met
aag agg ctg acc ttc tcc aca ggc act gag att ccg cat ttc ttc tgt
                                                                      337
Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys
                                105
gaa ctg gct cag gtc ctc aag gtg gcc cgc tct gat acc ctc ctc aat
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Glu Leu Ala Gln Val Leu Lys Val Ala Arg Ser Asp Thr Leu Leu Asn
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115 120 125

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gct Ala 145	ιGly	atc Ile	ctc Leu	ttc Phe	tcc Ser 150	tac Tyr	tct Ser	cag Gln	atc Ile	gtc Val 155	tcc Ser	tcc Ser	tta Leu	atg Met	aga Arg 160	481	
ato Met	tcc Ser	tcc Ser	acc Thr	gag Glu 165	ggc Gly	aag Lys	tac Tyr	aaa Lys	gcc Ala 170	ttt Phe	tcc Ser	acc Thr	tgt Cys	gga Gly 175	tct Ser	529	
cac His	ctc Leu	tgt Cys	gtg Val 180	gtc Val	tcc Ser	ttg Leu	ttc Phe	aat Asn 185	gga Gly	aca Thr	gga Gly	ctt Leu	999 Gly 190	gtc Val	tat Tyr	577	
ctc Leu	agt Ser	tct Ser 195	gct Ala	gtg Val	acc Thr	cat His	tct Ser 200	tcc Ser	cag Gln	agc Ser	agc Ser	tcc Ser 205	atg Met	gcc Ala	tca Ser	625	
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Tyr 65	Ala	Val	Ile	Met	Asn 70	Pro	His	Leu	Cys	Gly 75	Leu	Leu	Val	Leu	Ala 80		
Ser	Trp	Phe	Ile	Ile 85	Phe	Trp	Val	Ser	Leu 90	Val	His	Ile	Leu	Leu 95	Met		
Lys	Arg	Leu	Thr 100	Phe	Ser	Thr		Thr 105	Glu	Ile	Pro	His	Phe 110	Phe	Cys		

Glu Leu Ala Gln Val Leu Lys Val Ala Arg Ser Asp Thr Leu Leu Asn 115 120 125

Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val 130 135 140

Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg 145 150 155 160

Met Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Cys Val Val Ser Leu Phe Asn Gly Thr Gly Leu Gly Val Tyr 180 185 190

Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser Met Ala Ser 195 200 205

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<sup>&</sup>lt;211> 648

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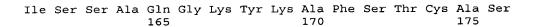
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241

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gat Asp	gtg Val 130	gtg Val	atg Met	tat Tyr	ttg Leu	gca Ala 135	gct Ala	atg Met	ctg Leu	ctg Leu	ggc Gly 140	Gly	ggt	ccc Pro	ctc Leu	433
aca Thr 145	GIA	att Ile	att Ile	tac Tyr	tct Ser 150	tac Tyr	tct Ser	aag Lys	ata Ile	gtt Val 155	tcc Ser	tcc Ser	ata Ile	cgt Arg	gca Ala 160	481
atc Ile	tca Ser	tca Ser	gct Ala	cag Gln 165	gly aaa	aag Lys	tac Tyr	aag Lys	gcg Ala 170	ttt Phe	tcc Ser	acc Thr	tgt Cys	gca Ala 175	tct Ser	529
cac His	atc Ile	tta Leu	att Ile 180	gtc Val	tcc Ser	tta Leu	ttt Phe	tat Tyr 185	ggt Gly	aca Thr	ctc Leu	cta Leu	ggt Gly 190	gtg Val	tac Tyr	577
ctt Leu	agt Ser	tct Ser 195	gct Ala	gca Ala	act Thr	Gly	aac Asn 200	tca Ser	cat His	tca Ser	ggt Gly	gct Ala 205	gca Ala	gcc Ala	ttg Leu	625
gtg Val	atg Met 210	tac Tyr	act Thr	gtg Val	Val	acc Thr 215	ccc Pro		,							649
<210 <211 <212 <213	> 2 > P	31 16 RT aimi	ri b	oliv	iens	is										
<220 <221 <222 <223	> m > (	1)	feat: (649) = 2	)	; gei	ne =	SBO	29;	Acce	ssio	n DD	BJ/E	MBL/	GenB	ank =	= AF127899
<400 Phe 1	> 1	31	Ile (					Thr '								
Asn	Ile (	Gln :	Thr F 20	His S	Ser I	iys V		[le ' 25	Thr 1	Phe I	Ala		Cys 30	Ile	Thr	
Gln :	Ile (	31y 1 35	His C	Cys I	eu I	eu F 4	he A	Ala A	Ala I	Leu A		Ile : 45	Phe 1	Met :	Leu	
Thr '	Val N 50	Met A	Ala T	'yr A	sp A	rg T	'yr V	al A	Ala I		Cys I	His 1	Pro I	Leu l	His	

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Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val
Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro Arg Phe Phe Cys
Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn
Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu
Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
                                          155
                     150
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
                 165
                                      170
His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
             180
Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Gly Ala Ala Ala Leu
Val Met Tyr Thr Val Val Thr Pro
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Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
                                                                           49
                                                                           97
aat atc cag aca cac agc aaa gtc atc acc ttt gca gac tgc atc acc
Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Asp Cys Ile Thr
                                                                          145
cag ata ggc cat tgc cta ctc ttt gca gca ttg gac atc ttt atg ctg
Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu
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40 4.5 35 193 act gtg atg gcc tat gac cgg tat gtg gcc acc tgt cac ccc ctg cac Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys His Pro Leu His tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca 241 Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala 75 tcc tgg atc ctg agt gcc ctg aat tcc tca tta caa ccc tta ata gtg 289 Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Pro Leu Ile Val ctg cgg ctt tcc ttc tgc aca gac ttg gaa atc ccc cac ttt ttc tgc 337 Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys 100 105 110 gaa ctt aat cag gtc ata cat ctt gcc tgt tat gac act ttc ctt aat 385 Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn 115 120 gat gtg gtg atg tat ttg gca gct atg ctg ctg ggc ggt ggt ccc ctc 433 Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Pro Leu 135 aca gga att att tac tct tac tct aag ata gtt tcc tcc ata cgt gca 481 Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 150 155 atc tca tca gct cag ggg aag tac aag gcg ttt tcc acc tgt gca tct 529 Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 165 cac atc tta att gtc tcc tta ttt tat ggt aca ctc cta ggt gtg tac 577 His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 180 185 ctt agt tot got goa act ggo aac toa cat toa agt got goa goo ttg 625 Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu 200 gtg atg tac aca gtg gtc acc ccc Val Met Tyr Thr Val Val Thr Pro 649 <210> 133 <211> 216 <212> PRT

<213> Saimiri boliviensis

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<221> misc\_feature

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Taxon = 27679; gene = SBO30; Accession DDBJ/EMBL/GenBank = AF127900

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Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Asp Cys Ile Thr 20 25 3.0

- Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu
- Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys His Pro Leu His 55
- Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
- Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Pro Leu Ile Val
- Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys 105 100
- Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn 120
- Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Pro Leu 130
- Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 150
- Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
- His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 185
- Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu 200
- Val Met Tyr Thr Val Val Thr Pro 210
- <210> 134 <211> 649
- <212> DNA
- <213> Saimiri sciureus
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- <221> CDS
- <222> (2)..(649)
- <223> Product = olfactory receptor
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<400> 135

10 15 97 aat atc cag aca cac agc aaa gtc atc acc ttt gca ggc tgc atc acc Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr 145 cag ata ggc cat tgc cta ctc ttt gca gca ttg gac atc ttt atg ctg Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu act gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac ccc ctg cac 193 Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His 50 241 tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala 65 70 289 tcc tgg atc ctg agt gcc ctg aat tcc tca tta caa acc tta ata gtg Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val 90 85 ctq cqq ctt tcc ttc tqc aca qac ttq qaa atc ccc cac ttt ttc tgc 337 Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys 385 gaa ctt aat cag gtc ata cat ctt gcc tgt tat gac act ttc ctt aat Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn 120 gat gtg gtg atg tat ttg gca gct atg ctg ctg ggc ggt ggt ccc ctc 433 Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu 135 aca gga att att tac tct tac tct aag ata gtt tcc tcc ata cgt gca 481 Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 145 529 atc tca tca gct cag ggg aag tac aag gcg ttt tcc acc tgt gca tct Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 165 170 cac atc tta att gtc tcc tta ttt tat ggt aca ctc cta ggt gtg tac 577 His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 185 180 ctt agt tct gct gca act ggc aac tca cat tca agt gct gca gcc ttg 625 Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu 195 200 205 gtg atg cac aca gtg gtc acc ccc 649 Val Met His Thr Val Val Thr Pro <210> 135 <211> 216 <212> PRT <213> Saimiri sciureus <220> misc\_feature <221> <222> (1)..(649) Taxon = 9521; gene = SSC31; Accession DDBJ/EMBL/GenBank = AF127901

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Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
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- Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
- Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu 40
- Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
- Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
- Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val 90
- Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys 105
- Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn 125
- Asp Val Val Met Tyr Leu Ala Ala Met Leu Gly Gly Gly Pro Leu
- Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
- Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 170
- His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 185
- Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu 195
- Val Met His Thr Val Val Thr Pro 215 210
- <210> 136 <211> 646
- <212> DNA
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			a gtc ccc agg ac r Val Pro Arg Th	
Asn Ile Gln 7			tat gcg agc tgc Tyr Ala Ser Cys 30	
			atg gaa gac acg Met Glu Asp Thr 45	
			atc tgt cac ccc Ile Cys His Pro 60	
_	_	Arg Leu Cys	ggc ttc tta gtg Gly Phe Leu Val 75	
_	_	_	gtg cac aat ttg Val His Asn Leu	_
Leu Gln Phe S			att tct aat ttc Ile Ser Asn Phe 110	
			tct gac acc ttt Ser Asp Thr Phe 125	
_	_		ttt ggt ttt ctt Phe Gly Phe Leu 140	
		Tyr Lys Ile	gcc tcc tcc att Ala Ser Ser Ile 155	
_	2 222 2	-	ttc tcc acc tgt Phe Ser Thr Cys	-
His Leu Ala V			aca gtt att gga Thr Val Ile Gly 190	
			agt gtg gtg gcc Ser Val Val Ala 205	
	gtg gtc act ccc Val Val Thr Pro 215			646

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<213> Saimiri sciureus
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<220>

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<222> (1)..(646)

<223> Taxon = 9521; gene = SSC32; Accession DDBJ/EMBL/GenBank = AF127902

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Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Arg Thr Ile Val
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Asn Ile Gln Thr His Ser Arg Val Ile Ala Tyr Ala Ser Cys Leu Thr 20 25 30

Gln Val Ser Phe Ser Ile Phe Phe Ala Cys Met Glu Asp Thr Leu Leu 35 40 45

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Phe Leu Val Leu Val 65 70 75 80

Ser Val Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val 85 90 95

Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys
100 105 110

Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn 115 120 125

Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile 130 135 140

Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Ser Ser Ile Leu Arg . 145 150 150 155 160

Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser 165 170 175

His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr 180 185 190

Leu Gly Ser Ser Met Ala Ser Pro Arg Lys Ser Val Val Ala Ser Val 195 200 205

Met Tyr Thr Val Val Thr Pro 210 215

<210> 138 <211> 649

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       Taxon = 9521; gene = SSC33; Accession DDBJ/EMBL/GenBank = AF127903
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<223> Product = olfactory receptor
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                                                                          49
 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln
                                        10
aac atg cag agc caa gac cca tcc atc ccc tat gcg ggc tgc ctg acc
                                                                         97
Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr
cag atg tac ttc ttc ttg tat ttt tcg gat cta gag agc ttc ctc ctt
                                                                         145
Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser Phe Leu Leu
gtg gcc atg gcc tat gac cgc tac gtg gcc atc tgc ctc ccc cta cat
                                                                        193
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu His
                         55
tac gcc acc atc atg agc ccc atg ctg tct cgc tcc ctg gtg gcg ctg
                                                                        241
Tyr Ala Thr Ile Met Ser Pro Met Leu Ser Arg Ser Leu Val Ala Leu
                     70
tcc tgg gtg ctg acc acc ttc cat gcc atg ttg cac act tta ctc atg
                                                                        289
Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
gcc agg ttg cgt ttt tgt gca gac aat gtg atc ctc cac ttt ttc tgt Ala Arg Leu Arg Phe Cys Ala Asp Asn Val Ile Leu His Phe Phe Cys
                                                                        337
            100
                                 105
                                                      110
gat atg tct gct ctg ctg aag ctg gcc tgc tct gac act cga gtt aat
                                                                        385
Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn
        115
                             120
                                                  125
gaa ttg gtg ata ttt atc atg gga ggc ctc att ctt gtc atc cca ctt
                                                                        433
Glu Leu Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Leu
    130
                         135
                                              140
cta ctt atc att ggg tcc tac gca cga att gtc ttc tcc atc ctc aag
                                                                        481
Leu Leu Ile Ile Gly Ser Tyr Ala Arg Ile Val Phe Ser Ile Leu Lys
gtc cct tct tct aag ggt atc tgc aag gcc gtc tct act tgt ggc tcc
                                                                        529
Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Val Ser Thr Cys Gly Ser
                165
                                     170
cac ctc tct gtg gtg tca ctg ttc tat ggg act gtt att ggt ctc tac
                                                                        577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr
tta tgc cca tca gct aat aat tct act cta aag gag act gtc atg gct
                                                                        625
Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Glu Thr Val Met Ala
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                                                  205
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gtg atg tac act gtg atg gcc ccc
Val Met Tyr Thr Val Met Ala Pro
   210
                        215
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<210> 139 <211> 216 <212> PRT

<213> Saimiri sciureus

<220>

<221> misc\_feature <222> (1)..(649)

<223> Taxon = 9521; gene = SSC33; Accession DDBJ/EMBL/GenBank = AF127903

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Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr

Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser Phe Leu Leu 35 40

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu His

Tyr Ala Thr Ile Met Ser Pro Met Leu Ser Arg Ser Leu Val Ala Leu

Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met 90

Ala Arg Leu Arg Phe Cys Ala Asp Asn Val Ile Leu His Phe Phe Cys 105

Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn

Glu Leu Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Leu 130

Leu Leu Ile Ile Gly Ser Tyr Ala Arg Ile Val Phe Ser Ile Leu Lys 145 150 160

Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Val Ser Thr Cys Gly Ser 165 170

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr 180 185

Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Glu Thr Val Met Ala 195 200

## Val Met Tyr Thr Val Met Ala Pro 210 215

<210> 140 <211> 646 <212> DNA <213> Saimiri sciureus	
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<220> <221> CDS <222> (2)(646) <223> Product =olfactory receptor	
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aac att caa act cac age aga gtc atc gcc tat gcg agc tgc ctg aca Asn Ile Gln Thr His Ser Arg Val Ile Ala Tyr Ala Ser Cys Leu Thr 20 25 30	7
cag atg tct ttt tca atc ttt ttt gcg tgt atg gaa gac acg ctc ctg Gln Met Ser Phe Ser Ile Phe Phe Ala Cys Met Glu Asp Thr Leu Leu 35 40 45	5
gct gtg atg gcc tat gac cgg ttt gtt gcc atc tgt cac ccc ctg cac Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60	3
tac cca gtc atc atg aac cca cga ctc tgt ggc ttc tta gtg ttg gtg Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Phe Leu Val Leu Val 65 70 75 80	1
tct gtt ttt ctt agc ctt tta ata tcc cag gtg cac aat ttg att gtc Ser Val Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val 85 90 95	9
tta caa ttt tct tgc ttc aaa gag ata aag att tct aat ttc ttc tgt Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys 100 105 110	7
gac cct tct caa ctc ctc acc ctt tct tgt tct gac acc ttt gtc aat Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn 115 120 125	5
aac ata gtc acg aat ttc ttt gct gct gta ttt ggt ttt ctt ccc atc Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile 130 135 140	3
tca ggg atc ttt ttc tct tac tat aaa att gcc tcc tcc att ctg aga Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Ser Ser Ile Leu Arg 145 150 155 160	1
gtt cca tta tca agt ggg aag tat aaa gcc ttc tcc acc tgt agc tct Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser 165 170 175	9

cac ctg gca gtt gtt tgc tta ttt tat gga aca gtc att gga gtg tac His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr 180 185 190
ctt ggg tca tca atg gca tcc ccc agg aag agt gtg gtg gcc tca gtg Leu Gly Ser Ser Met Ala Ser Pro Arg Lys Ser Val Val Ala Ser Val 195 200 205
atg tac aca gtg gtc act ccc  Met Tyr Thr Val Val Thr Pro 210 215
<210> 141 <211> 215 <212> PRT <213> Saimiri sciureus
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Asn Ile Gln Thr His Ser Arg Val Ile Ala Tyr Ala Ser Cys Leu Thr 20 25 30
Gln Met Ser Phe Ser Ile Phe Phe Ala Cys Met Glu Asp Thr Leu Leu 35 40 45
Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 60
Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Phe Leu Val Leu Val 65 70 75 80
Ser Val Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val 85 90 95
Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys 100 105 110
Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn 115 120 125
Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile 130 135 140
Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Ser Ser Ile Leu Arg 145 150 155 160
Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser 165 170 175

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His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr
            180
                                185
Leu Gly Ser Ser Met Ala Ser Pro Arg Lys Ser Val Val Ala Ser Val
        195
                            200
                                                205
Met Tyr Thr Val Val Thr Pro
    210
                        215
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= AF127905
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ggaagacaga agcatctcct tcacaggatg cgtcatgcaa ttcttttttg ccagcatatt
                                                                     120
tgtggtgaca gaaatattca tgctggcagt gatggcctat gacagatttg tggtggtgtg
                                                                     180
ttaccetetg ctctacacag ttgcaatgte ccagaggett ttetttttgt tagtggetae
                                                                     240
atcatacttc agggtgacag tctgtttctt gacaattacc ttctttctcc tggaattatc
                                                                     300
cttcagagga aataatatca ttaataactt tqtqtqtqaq cctqctqcca ttqttqctqt
                                                                     360
gccatgcttt gacccctaca tgagccagga aatcattttc atttctgcca cattcaatga
                                                                     420
aacaagcagc ctgatgatca ttctcacctc ctaagatttc gtttttatca atgtcatgat
                                                                     480
gatgccttcc actgggggc gcataaaagc atgcgcgacc tgttcctccc agctgaccgc
                                                                     540
cattatcatt ttccatggga ccatctcttt tctctattgt gttcctaact ccaaaagttc
                                                                     600
atggctcatg gtcaaggtgg gctctatctt ttacacagtg gtcatcccc
                                                                     649
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<223> Product = olfactory receptor
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c tit gta gac atc tgt gtt acc tcc acc acg att cca aag aca cta tca
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Phe Val	. Asp Il	le Cys V 5	al Thr	Ser T	hr Ti		le P	ro L	ys Tl	nr Le		£	
aac atc c Asn Ile G	_		_				_		_	_			97
cag ttg t Gln Leu T 3													145
acc gtg a Thr Val M 50													193
tac atg g Tyr Met V 65		-			_		_	_	_	_			241
tcc tgg a Ser Trp I													289
tta tca c Leu Ser L	_	_	_	_							_		337
gaa ctt a Glu Leu A 1	_			Àla	_		_		_				385
aac ctg g Asn Leu V 130		_			_	_							433
gct ggg a Ala Gly I 145	_			_		_				_	_		481
atc tca t Ile Ser S													529
cac ctc t His Leu S	_	_			_								577
ctg agt t Leu Ser S 1				Ser									625
gtg atg t Val Met T 210													649
<210> 14 <211> 21 <212> PR <213> Sa	6 .T	oolivien	sis	·									
<222> (1	sc_feat )(649 xon = 2		ene = SI	3065;	Acce	essio	on DI	OBJ/E	EMBL,	/GenI	3ank =	= AF	127906

- Asn Ile Gln Thr His Ser Lys Val Ile Thr Tyr Ala Gly Cys Val Thr 20 25 30
- Gln Leu Tyr Phe Ser Val Leu Phe Ile Gly Leu Asp Ser Leu Leu Leu 35 40 45
- Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg 50 55 60
- Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Val 65 70 75 80
- Ser Trp Ile Met Ser Ala Leu His Ser Leu Thr Glu Ser Leu Met Ala 85 90 95
- Leu Ser Leu Leu Phe Cys Thr Asp Leu Lys Ile Leu His Phe Cys 100 105 110
- Glu Leu Asn Gln Ile Ile His Ile Ala Cys Ser Asp Thr Cys Leu Asn 115 120 125
- Asn Leu Val Met Tyr Leu Ser Ala Val Leu Leu Gly Gly Pro Leu 130 135 140
- Ile Ser Ser Ala Lys Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 165 170 175
- His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Leu Gly Val Tyr 180 185 190
- Leu Ser Ser Ala Ala Thr His Asn Ser Leu Ser Ser Thr Ala Ala Ser 195 200 205
- Val Met Tyr Thr Val Val Thr Pro
- <210> 145
- <211> 649
- <212> DNA
- <213> Saimiri sciureus
- <220>
- <221> misc\_feature
- <222> (1)..(649)
- <223> Taxon = 9521; gene = SSC69; Accession DDBJ/EMBL/GenBank = AF127907

<221 <221 <221	1 > ( 2 >	CDS (2). Produ			facto	ory :	recej	ptor								
	t gt									ar V					tg gta eu Val	49
					agc Ser											97
					cta Leu											145
					gac Asp											193
					aac Asn 70											241
					gcc Ala											289
ctg Leu	cgg Arg	ctt Leu	tcc Ser 100	ttc Phe	tgc Cys	aca Thr	gac Asp	ttg Leu 105	gaa Glu	atc Ile	ccc Pro	cac His	ttt Phe 110	ttc Phe	tgc Cys	337
_			_	_	ata Ile			-	_		_					385
_			_		ttg Leu	_	-	_	_	_						433
					tct Ser 150											481
					Gly aaa											529
				_	tcc Ser											577
					act Thr											625
					gtc Val											649

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Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val

Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr

Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His

Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala

Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Pro Leu Ile Val 85 90

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys 105

Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn

Asp Val Val Met Tyr Leu Ala Ala Met Leu Gly Gly Gly Pro Leu

Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser

His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Ala Tyr 180

Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu 195 200

Val Met Tyr Thr Val Val Thr Pro 210 215

<210> 147

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<213> Papio hamadryas
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<222>
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       Product = olfactory receptor
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t gtg gcc atc tgc ttc ccc ctg cac tac acc gcc atc atg agc ccc atg
                                                                              49
  Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
ctc tgt ctc gcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat
Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
                                                                             97
                                   25
gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac
                                                                            145
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
        35
                               40
aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg
                                                                            193
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
    50
                          55
gcc tgc tct gac act cga gtc aat gaa ttg gtg ata ttt atc atg gga
                                                                            241
Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
ggg ctg att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca
                                                                            289
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
                                       90
cgg att gtc tcc tcc atc ctc aag gtc cct tcg tct aag ggt atc tgc
                                                                            337
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
             100
aag geg tte tet act tgt gge tee cae ete tet gtg gtg tea etg tte
                                                                            385
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
        115
                               120
tat ggg acc att att ggt ctc tac ttc tgc cca tca gct aat agt tct
                                                                            433
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser
act cta aag gag act gtt atg gct atg atg tac act gtg gtg acc ccc Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
                                                                            481
                                            155
                                                                  160
atg ctq
                                                                            487
Met Leu
```

<sup>&</sup>lt;210> 148

<sup>&</sup>lt;211> 162

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Papio hamadryas

<400> 149

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Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
                                     10
Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
                                105
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
        115
                            120
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser
Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
                                        155
Met Leu
<210> 149
<211> 486
<212> DNA
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      CDS
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      (2)..(484)
<222>
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Val Ala : 1	lle Cys G 5		eu His T	yr Ser T 10	hr Leu L		ro Trp 5
gcc tgc ato Ala Cys Met							
gcc acc acc Ala Thr Thi 35							
cca atc atc Pro Ile Ile 50					_		_
gca agt gct Ala Ser Ala 65							
gta gtc ttc Val Val Phe							
cgc atc cto Arg Ile Lev				Ala Ser			
aag gtc ttc Lys Val Phe 115	Ser Thr						
ttt gga aca Phe Gly Thr 130							
gtt acc aca Val Thr Thr 145							
atg ct Met							486
<210> 150 <211> 161 <212> PRT <213> Papi	o hamadr	yas					
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Ala Cys Met	Ala Met 20	Val Gly	Thr Ser 25	Trp Leu	Thr Gly	Ile Ile 30	Thr
Ala Thr Thr	His Ala	Phe Leu	Ile Phe 40	Ser Leu	Pro Phe 45	Pro Ser	Arg

```
Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu
Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr
Val Val Phe Ile Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile
Arg Ile Leu Gly Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg
                                105
Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe
        115
                            120
                                                125
Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser
Val Thr Thr Asp Arg Val Leu Ser Val Phe Tyr Thr Val Ile Thr Pro
                    150
                                        155
Met
<210> 151
<211> 487
<212> DNA
<213> Papio hamadryas
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<223> Taxon = 9557; gene = PPA135; pseudogene; Accession DDBJ/EMBL/Genbank
= 179718
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tgtggacatc tgaagtccct tgcactaccc agtcatcatg aacgaaagaa cacgggccaa
                                                                      60
actggctgct gcttcctggt tcccaggctt tcctgtagct actgtgcaga ccacgtggct
                                                                      120
cttcagcttt ccattctgtg gcaccaacaa ggtgaaccac ttcttctgtg acagcccacc
                                                                      180
tgtgctgaag ctggtctgtg tagacacagc actgtttgag atctacacca tcactggaac
                                                                      240
cattetggtg gtcatgatec cetgettget gatettgtgt tectacacte teattgetge
                                                                      300
tgccatcctc aagatcccat cagctaaagg gaagcataaa gccttctcta cgtgatcctc
                                                                     360
acateteett gttgtetete ttttetatet ateattaaac eteacatatt tteageetaa
                                                                      420
atcaaataat teteetgaaa geaaaaaget getateattg ttetaeaetg ttgtgaetee
                                                                      480
                                                                      487
catgttg
```

<210> 152 <211> 482

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<212> DNA
<213> Papio hamadryas
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<222>
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= 179719
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                                                                       60
geteetetge ttgtgttggg ggetetetgt tetetatggt eteeteetea eteteeteet
                                                                      120
gaccagggtg accttctgtg ggactcaaga gatccactac ctcttctgtg agatgtacgt
                                                                      180
cetgetgeag etggeatgtt ceaacaccca catcattcac acagtgetgg ttgctactgg
                                                                      240
ctgctttctt cctcgacccc ttagggttca cgactacatc ctatatacgt attgtcagaa
                                                                      300
ccatccttca gataccctca gcctctaaga aacacaaaac cttctctgcc tgtgcctcac
                                                                      360
atttgggtgt ggtctccctc ttttatggga cacttgttat ggtatacctg cagccctcc
                                                                      420
acacctactc catgaaggac tcagtagcca cagtgatgta tgctgtggtg acacctatga
                                                                      480
                                                                      482
tq
<210>
       153
<211>
       481
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      DNA
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      Papio hamadryas
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<223>
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c ctg gca ata tgt caa ccc ctg cgc tac cca gtg ctc atg aat ggg agg
                                                                       49
 Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg
tta tgc aca gtc ctt gtg gct gga gct tgg gtc gcc ggc tcc att cat
                                                                       97
Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Ile His
ggg tet ate cag gee ace etg ace tte ege eta ece tat tgt ggg ece
                                                                      145
Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
                            40
aat cag gta gat tac ttt atc tgt gac atc cct gca gta ttg aga ctg
                                                                      193
Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu
                        55
                                            60
gcc tgt gct gac aca act gtc aat gag ctt gtg acc ttt gtg gac atc
                                                                      241
Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile
65
                    70
                                        75
                                                             80
gga gta gtg gcc gcc agt tgc ttc atg tta att cta ctt tcc tat gcc
                                                                      289
```

Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala 85 90 95	
aac ata gtc cat gcc atc ctg aag ata cgc acc act gat ggg agg cgc Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg Arg 100 105 110	
cgg gcc ttc tct acc tgt ggc tcc cac cta act gtg gtc aca gtc tac Arg Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Thr Val Tyr 115 120 125	
tat gtt ccc tgt att ttc atc tac ctt agg gct ggc tcc aag agc ccc Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Ser Pro 130 140	
ctg gat ggg gca gtg gct gtg ttt tac act gtt gtc act cca ttc ctg Leu Asp Gly Ala Val Ala Val Phe Tyr Thr Val Val Thr Pro Phe Leu 145 150 155 160	
<210> 154 <211> 160 <212> PRT <213> Papio hamadryas	
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<400> 154 Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg 1 5 10 15	
Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Ile His 20 25 30	
Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro 35 40 45	
Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu 50 55 60	
Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile 65 70 75 80	
Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala 85 90 95	
Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg Arg 100 105 110	
Arg Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Thr Val Tyr 115 120 125	
Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Ser Pro 130 135 140	

145 150 155 160	
<210> 155 <211> 487 <212> DNA <213> Papio hamadryas	
<pre>&lt;220&gt; &lt;221&gt; misc_feature &lt;222&gt; (1)(487) &lt;223&gt; Taxon = 9557; gene = PPA138; Accession DDBJ/EMBL/GenBank = A</pre>	F179721
<220> <221> CDS <222> (2)(487) <223> Product = olfactory receptor	
<400> 155 t gta gcc ata tgc aaa cct tta ctt tat cca gtg att atg acc aat gga Val Ala Ile Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Thr Asn Gly 1 5 10 15	49
ctg tgc atc cgg cta tta gtc ttg tca ttt gta ggt ggc ttc ctt cat Leu Cys Ile Arg Leu Leu Val Leu Ser Phe Val Gly Gly Phe Leu His 20 25 30	97
gcc tta att cat gaa ggc att tta ttc aga tta acc ttc tgt aat tct Ala Leu Ile His Glu Gly Ile Leu Phe Arg Leu Thr Phe Cys Asn Ser 35 40 45	145
aac ata ata cat cac ttt tac tgt gac att atc cca ttg tta acg att Asn Ile Ile His His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Thr Ile 50 55 60	193
tcc tgt act gac cct tct att aat ttt tta atg ctt ttt att ttg tct Ser Cys Thr Asp Pro Ser Ile Asn Phe Leu Met Leu Phe Ile Leu Ser 65 70 75 80	241
ggt tca ata cag gta ttc act att ttg act gtt ctt gtc tct tat gca Gly Ser Ile Gln Val Phe Thr Ile Leu Thr Val Leu Val Ser Tyr Ala 85 90 95	289
ttt gtc ctc ttt aca atc tta aaa aaa aag tca gtc aaa ggc ata agg Phe Val Leu Phe Thr Ile Leu Lys Lys Lys Ser Val Lys Gly Ile Arg 100 105 110	337
aaa gcc ttt tcc acc tgt gga gcc cat ctc ttc tct gtc tgt tta tac Lys Ala Phe Ser Thr Cys Gly Ala His Leu Phe Ser Val Cys Leu Tyr 115 120 125	385
tat ggc ccc ctt ctc ttc atg tat gtg ggc cct gca tct cca caa gca Tyr Gly Pro Leu Leu Phe Met Tyr Val Gly Pro Ala Ser Pro Gln Ala 130 135 140	433
gat gat caa gat atg gta gag tgt gta ttt tac act gtc atc att cct Asp Asp Gln Asp Met Val Glu Cys Val Phe Tyr Thr Val Ile Ile Pro 145 150 155 160	481
ttc tta Phe Leu	487

Leu Asp Gly Ala Val Ala Val Phe Tyr Thr Val Val Thr Pro Phe Leu

<210> 156

<221> CDS

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<211> 162
<212> PRT
<213> Papio hamadryas
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Val Ala Ile Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Thr Asn Gly
Leu Cys Ile Arg Leu Leu Val Leu Ser Phe Val Gly Gly Phe Leu His
Ala Leu Ile His Glu Gly Ile Leu Phe Arg Leu Thr Phe Cys Asn Ser
Asn Ile Ile His His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Thr Ile
Ser Cys Thr Asp Pro Ser Ile Asn Phe Leu Met Leu Phe Ile Leu Ser
                    70
Gly Ser Ile Gln Val Phe Thr Ile Leu Thr Val Leu Val Ser Tyr Ala
Phe Val Leu Phe Thr Ile Leu Lys Lys Ser Val Lys Gly Ile Arg
                                105
Lys Ala Phe Ser Thr Cys Gly Ala His Leu Phe Ser Val Cys Leu Tyr
                            120
Tyr Gly Pro Leu Leu Phe Met Tyr Val Gly Pro Ala Ser Pro Gln Ala
    130
                        135
                                            140
Asp Asp Gln Asp Met Val Glu Cys Val Phe Tyr Thr Val Ile Ile Pro
Phe Leu
<210> 157
<211> 487
<212> DNA
<213> Papio hamadryas
<220>
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<223> Taxon = 9557; gene = PPA139; Accession DDBJ/EMBL/GenBank = AF179722
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<222> (2)..(487)
<223> Product = olfactory receptor
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                                                                        49
  Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Val Val Ser Arg Arg
ctc tqc ctc ctg ctg gtc tcc ctc aca tac ctc tat qqc ttt tct aca
                                                                        97
Leu Cys Leu Leu Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr
get att gtg gtt tea eet tgt ata tte tet atg tet tat tge tet tet
                                                                       145
Ala Ile Val Val Ser Pro Cys Ile Phe Ser Met Ser Tyr Cys Ser Ser
aat ata atc aat cat ttt tac tgt gat att gca cct ctg tta gca tta
                                                                       193
Asn Ile Ile Asn His Phe Tyr Cys Asp Ile Ala Pro Leu Leu Ala Leu
                        55
tot tgo tot gat act tac tta oca gaa goa ata gto tto ata tot goa
                                                                       241
Ser Cys Ser Asp Thr Tyr Leu Pro Glu Ala Ile Val Phe Ile Ser Ala
gca aca aat ttg gtt ttt tcc atg att aca gtt cta gta tct tat ttc
                                                                       289
Ala Thr Asn Leu Val Phe Ser Met Ile Thr Val Leu Val Ser Tyr Phe
aat att gtt ttg tcc att cta agg atg cat tca tca gaa gga agg aaa
                                                                      337
Asn Ile Val Leu Ser Ile Leu Arg Met His Ser Ser Glu Gly Arg Lys
            100
                                105
aaa gcc ttt tcc acc tgt gct tca cat atg atg gca gtc aca gtt ttc
                                                                      385
Lys Ala Phe Ser Thr Cys Ala Ser His Met Met Ala Val Thr Val Phe
        115
                            120
tat ggg aca atg ctg ttc atg tat ttg cag ccc caa acc aac cac tca
                                                                       433
Tyr Gly Thr Met Leu Phe Met Tyr Leu Gln Pro Gln Thr Asn His Ser
   130
ctg gat act gat aag atg gct tct gtg ttt tac aca ttg gtg att cct
                                                                      481
Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro
                    150
atg ctg
                                                                      487
Met Leu
<210> 158
<211> 162
<212>
      PRT
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<400> 158
Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Val Val Ser Arg Arg
                                    10
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Leu Cys Leu Leu Leu Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr

Ala	Ile	Val 35	Val	Ser	Pro	Cys	Ile 40	Phe	Ser	Met	Ser	Tyr 45	Суѕ	Ser	Ser		
Asn	Ile 50	Ile	Asn	His	Phe	Tyr 55	Cys	Asp	Ile	Ala	Pro 60	Leu	Leu	Ala	Leu		
Ser 65	Cys	Ser	Asp	Thr	Tyr 70	Leu	Pro	Glu	Ala	Ile 75	Val	Phe	Ile	Ser	Ala 80		
Ala	Thr	Asn	Leu	Val 85	Phe	Ser	Met	Ile	Thr 90	Val	Leu	Val	Ser	Tyr 95	Phe		
Asn	Ile	Val	Leu 100	Ser	Ile	Leu	Arg	Met 105	His	Ser	Ser	Glu	Gly 110	Arg	Lys		
Lys	Ala	Phe 115	Ser	Thr	Cys	Ala	Ser 120	His	Met	Met	Ala	Val 125	Thr	Val	Phe		
Tyr	Gly 130	Thr	Met	Leu	Phe	Met 135	Tyr	Leu	Gln	Pro	Gln 140	Thr	Asn	His	Ser		
Leu 145	Asp	Thr	Asp	Lys	Met 150	Ala	Ser	Val	Phe	Tyr 155	Thr	Leu	Val	Ile	Pro 160		
Met	Leu																
<210 <211 <212 <213	> 4 > E	159 187 DNA Papic	o han	nadry	as '												
<220 <221 <222 <223	.> π :> (	(1).	_feat .(487 n = 9	7)	ger	ne =	PPA1	40;	Acce	essic	on DI	OBJ/E	EMBL/	'GenE	Bank =	AF17:	9723
<220 <221 <222 <223	> C > (		.(487 1Ct =	7) = olf	acto	ory r	ecep	otor									
	g go									ır Āl					cc atg co Met	4	49 ·
													acc Thr			!	97

gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgc gca gac Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp

Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu 50 55 60	3
gcc tgc tct gac act cga gtc aat gaa ttg gtg ata ttt atc atg gga 24: Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly 65 70 75 80	L
ggg ctg att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca 289 Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala 85 90 95	€
cgg att gtc tcc tcc atc ctc aag gtc cct tcg tct aag ggt atc tgc Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys 100 105 110	7
aag gcg ttc tct act tgt ggc tcc cac ctc tct gtg gtg tca ctg ttc Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 115 120 125	5
tat ggg acc att att ggt ctc tac ttc tgc cca tca gct aat agt tct Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser 130 135 140	3
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atg ctg Met Leu	7
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<pre>&lt;212&gt; PRT &lt;213&gt; Papio hamadryas  &lt;220&gt; &lt;221&gt; misc_feature &lt;222&gt; (1)(487) &lt;223&gt; Taxon = 9557; gene = PPA140; Accession DDBJ/EMBL/GenBank = AF1797 &lt;400&gt; 160 Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met</pre>	723
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Arg	Ile	Val	Ser 100	Ser	Ile	Leu	Lys	Val 105	Pro	Ser	Ser	Lys	Gly 110	Ile	Cys	
Lys	Ala	Phe 115	Ser	Thr	Cys	Gly	Ser 120	His	Leu	Ser	Val	Val 125	Ser	Leu	Phe	
Tyr	Gly 130	Thr	Ile	Ile	Gly	Leu 135	Tyr	Phe	Cys	Pro	Ser 140	Ala	Asn	Ser	Ser	
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Met	Leu															
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	tgt Cys															97
	Gly aaa															145
	gtc Val 50		_		_	_	-	_		_					_	193
acc		aca	~~~					~~~					~~~			
	Cys			act Thr												241

atc atc ctg tgc tcc cta agg act cat atc tct gaa ggg cgt cac aaa Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys 100 105 110

gct ctg tct agt tgt acc tct cat atc ttt gtt gtc atc tta ttc ttt Ala Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe 115 120 125	
gtc cct tgt tca tac ctg tat cta aga cct cta acc tcc ttc ccc act  Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Pro Thr  130  140	
gac aaa gct gtg act gtg ttt tgc acc cta ttt aca cct atg ttg 478 Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu 145 150 155	
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Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His 20 25 30	
Gly Gly Ile Gln Thr Leu Phe Ile Ala Gln Leu Pro Phe Cys Gly Pro 35 40 45	
Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu 50 55 60	
Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser 65 70 75 80	
Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val 85 90 95	
Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys 100 105 110	
Ala Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe 115 120 125	
Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Pro Thr 130 135 140	
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                                      10
gto tgo aca ctg ctt gtt ttt act tct tgg ctg gtt tca ttc tta atc
                                                                       97
Val Cys Thr Leu Leu Val Phe Thr Ser Trp Leu Val Ser Phe Leu Ile
            20
ata ttc cca gca ctc atg ttg ctc tta cag ctt gat tac tgt agg tct
                                                                      145
Ile Phe Pro Ala Leu Met Leu Leu Leu Gln Leu Asp Tyr Cys Arg Ser
aat att atg gac cat ttt acc tgt gat tat ttt ccc ctg ctg caa ctt
                                                                      193
Asn Ile Met Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
                        55
gct tgt tca gac aca aaa ttc cta gag gtg atg gga ttt tct tgt gct
                                                                      241
Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Gly Phe Ser Cys Ala
gtg ttt act cta atg ttg act ttg gca tta ata ttt ctg tcc tac ata
                                                                      289
Val Phe Thr Leu Met Leu Thr Leu Ala Leu Ile Phe Leu Ser Tyr Ile
                85
tac att atc aga aca att ttg aga att cct tct gct agt caa agg aca
                                                                      337
Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Thr
aag goo ttt too aca tgt tot too cac atg att gto atc too atc tot
                                                                      385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
                            120
tat ggc agc tgc att ttt atg tac att aaa ccc tca gca aaa gat aga
                                                                      433
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
                        135
gtg tcc ttg agc aag gga gtg gca ata cta aac acc tca gta gcc ccc
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Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Āla Pro
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atg ctg
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Met Leu
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Ile Phe Pro Ala Leu Met Leu Leu Gln Leu Asp Tyr Cys Arg Ser
Asn Ile Met Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Gly Phe Ser Cys Ala
                    70
Val Phe Thr Leu Met Leu Thr Leu Ala Leu Ile Phe Leu Ser Tyr Ile
                85
                                    90
Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Thr
            100
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Ala Pro
Met Leu
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 Val Ala Ile Cys Gln Pro Leu His Tyr Ser Thr Leu Leu Ser Pro Trp
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1				5					10	כ				15	5	
													atc Ile 30			97
													ccc Pro			145
													ctg Leu			193
													aca Thr			241
													tct Ser			289
-		-		_				_	_			_	agc Ser 110	_	_	337
_	-				_				_			_	tct Ser			385
			_	_						_	_	_	ggc Gly			433
													atc Ile			481
atg Met																487
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Ala	Cys	Met	Ala 20	Met	Val	Gly	Thr	Ser 25	Trp	Leu	Thr	Gly	Ile 30	Ile	Thr	

Ala Thr Thr His Ala Phe Leu Ile Phe Ser Leu Pro Phe Pro Ser Arg 35 40 40

Pro	Ile 50	Ile	Pro	His	Phe	Leu 55	Сув	Asp	Ile	Leu	Pro 60	Val	Leu	Arg	Leu	
Ala 65	Ser	Ala	Gly	Lys	His 70	Arg	Ser	Glu	Ile	Ser 75	Val	Met	Thr	Ala	Thr 80	
Val	Val	Phe	Ile	Met 85	Ile	Pro	Phe	Ser	Leu 90	Ile	Val	Thr	Ser	Tyr 95	Ile	
Arg	Ile	Leu	Gly 100	Ala	Ile	Leu	Ala	Met 105	Ala	Ser	Thr	Gln	Ser 110	Arg	Arg	
Lys	Val	Phe 115	Ser	Thr	Сув	Ser	Ser 120	His	Leu	Leu	Val	Val 125	Ser	Leu	Phe	
Phe	Gly 130	Thr	Ala	Ser	Ile	Thr 135	Tyr	Ile	Arg	Pro	Gln 140	Ala	Gly	Ser	Ser	
Val 145	Thr	Thr	Asp	Arg	Val 150	Leu	Ser	Leu	Phe	Tyr 155	Thr	Val	Ile	Thr	Pro 160	
Met	Leu															
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					gtg Val											97
					tta Leu											145
					ttt Phe											193
					cga Arg 70											241

Gly Leu Ile Val Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala 85 90 95	
aga att gtc tcc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc  Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys  100  105  110	
aag gcc ttg tct act tgt ggc tcc cac ctg tct gtg gtg tca ctg ttc 385 Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 115 120 125	
tat ggg acc gtt att ggt ctc tac tta tgc cca tca gct aat agt tct 433  Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser  130 135 140	
act cta aag gac act gtc atg gct atg atg tac act gtg gtg acc ccc  Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro  145  150  160	
atg ctg Met Leu	
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Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe

115 120 125

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser 130 135 140

Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro 145 150 155 160

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  Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
ctc tgt ctc tcc gtg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat
                                                                          97
Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
                                 25
gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac
                                                                         145
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
                             40
aat gtg atc ccc cac ttt ttc tgt gat atg tct gct cta ctg aag ctg
                                                                         193
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
    50
gcc tgc tct gac act cga gtt aat gaa tgg gtg ata ttt atc atg gga Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
                                                                         241
ggg ctc att gtt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca
                                                                         289
Gly Leu Ile Val Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
                                      90
aga att gtc tcc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc
                                                                         337
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
            100
                                 105
aag gee ttg tet aet tgt gge tee eac etg tet gtg gtg tea etg tte
                                                                         385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
        115
                             120
tat ggg acc gtt att ggt ctc tac tta tgc cca tca gct aat aqt tct
Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser
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Met Leu

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gttgctaagc atttcatatg taattggttt cctgcatcct ctggttcatg tgagtttact
                                                                      120
attgegaeta aetttetgea ggtttaacat aatacattat ttetaetgtg aaattttaca
                                                                      180
actgttcaaa atttcatgca atggtccatc tattaacgca ctaatgatat ttatttttgg
                                                                      240
tgcttttata caaataccca ctttaatgac gatcataatc tcttatactc gtgtgctctt
                                                                      300
tgatattetg aaaaaaaagt etgaaaaggg cagaagcaaa geetteteca catgeagege
                                                                      360
ccatctgctt tctgtctcat tgtactacgg aactctgatc ttcatgtatg tgcgtcctgc
                                                                      420
atctggetta getgaagace cagacaaagt gtattetett ttacaegatt ataatteece
                                                                      480
tgcta
                                                                      485
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                                                                       49
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gto tgt goo cta atg ott goa ttg tgo tgg gto oto acc aat atc att
                                                                       97
Val Cys Ala Leu Met Leu Ala Leu Cys Trp Val Leu Thr Asn Ile Ile
gee etg act cae acg tte etc atg get egg ttg tee tte tgt gtg act
                                                                      145
Ala Leu Thr His Thr Phe Leu Met Ala Arg Leu Ser Phe Cys Val Thr
        35
                            40
ggg gaa att gct cac ttt ttc tgt gac atc act cct gtc ctg aag ctg
                                                                      193
Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
                        55
tca tgt tct gac acc cac atc aac gag atg atg gtt ttt gtc ttg gga
                                                                      241
Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
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75

Gly Thr Val	ctc atc Leu Ile 85	gtc co Val Pi	cc ttt co Phe	tta Leu	tgc Cys 90	att Ile	gtc Val	acc Thr	tcc Ser	tac Tyr 95	atc Ile	289
cac att gto His Ile Val	cca gct Pro Ala 100	atc ct lle Le	g agg eu Arg	gtc Val 105	cga Arg	acc Thr	cgt Arg	ggt Gly	999 Gly 110	gtg Val	ggc Gly	337
aag gcc ttt Lys Ala Phe 115	Ser Thr	tgc ag Cys Se	gt tcc er Ser 120	cac His	ctc Leu	tgc Cys	gtt Val	gtt Val 125	tgt Cys	gtg Val	ttc Phe	385
tat ggg acg Tyr Gly Thr 130			a Tyr									433
gaa gag aag Glu Glu Lys 145												481
atg ttg Met Leu												487
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<pre>&lt;222&gt; (1). &lt;223&gt; Taxo &lt;400&gt; 173 Val Ala Ile 1  Val Cys Ala  Ala Leu Thr</pre>	(487) n = 9598  Cys Arg 5  Leu Met 20  His Thr	; gene Pro Le Leu Al Phe Le	u Cys a Leu u Met 40 e Cys	Tyr Cys 25 Ala	Ser 10 Trp	Thr Val Leu	Val Leu Ser	Thr Thr Phe 45	Arg Asn 30 Cys	Pro 15 Ile Val	Gln Ile Thr	AF179730
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Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Val Val Cys Val Phe 115 120 125

Tyr	Gly	Thr	Leu	Phe	Ser	Ala	Tyr	Leu	Cys	Pro	Pro	Ser	Ile	Ala	Ser
	130					135			-		140				

Glu Glu Lys Asp Ile Ala Ala Ala Ala Met Tyr Thr Ile Val Thr Pro 145 150 155 160

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                                                                       49
  Val Ala Ile Cys His Pro Leu His Tyr Ser Thr Ile Met Ala Leu Arg
ctc tgt gcc tct ctg gta gct gca cct tgg gtc att gcc att ttg aac
                                                                       97
Leu Cys Ala Ser Leu Val Ala Ala Pro Trp Val Ile Ala Ile Leu Asn
cct ctc ttg cac act ctt atg atg gcc cat ctg cac ttc tgc tct gat
                                                                      145
Pro Leu His Thr Leu Met Met Ala His Leu His Phe Cys Ser Asp
                            40
aat gtt atc cac cat ttc ttc tgt gat atc aac tct ctc ctc cct ctg
                                                                      193
Asn Val Ile His His Phe Phe Cys Asp Ile Asn Ser Leu Leu Pro Leu
                        55
tee tgt tee aac acc agt ett aat cag ttg agt gtt etg get acg gtg
                                                                      241
Ser Cys Ser Asn Thr Ser Leu Asn Gln Leu Ser Val Leu Ala Thr Val
                    70
ggg ctg atc ttt gtg gta cct tca gtg tgt atc ctg gta tcc tat atc
                                                                      289
Gly Leu Ile Phe Val Val Pro Ser Val Cys Ile Leu Val Ser Tyr Ile
                85
ctc att gtt tct gct gtg atg aaa gtc cct tct gcc caa gga aaa ctc
                                                                      337
Leu Ile Val Ser Ala Val Met Lys Val Pro Ser Ala Gln Gly Lys Leu
            100
aag gct ttc tct atc tgt gga tct cac ctt gcc ttg gtc att ctt ttc
                                                                      385
Lys Ala Phe Ser Ile Cys Gly Ser His Leu Ala Leu Val Ile Leu Phe
tat gga gca atc aca ggg gtc tat atg agc ccc tta tcc aat cac tct
                                                                      433
Tyr Gly Ala Ile Thr Gly Val Tyr Met Ser Pro Leu Ser Asn His Ser
                       135
                                            140
```

ac Th 14	r Glı	a aaa u Lys	a gad s Asp	c tc p Se:	a gco r Ala 150	a Ala	tca Sei	a gto r Val	att   Ile	ttt Phe 155	e Met	g gtt Val	gta Val	a gca L Ala	a cct a Pro 160		4	481
_	g ttg l Lei	-															4	187
<2 <2	10> 11> 12> 13>	175 162 PRT Pan	trog	jlodj	/tes													
<2: <2:	20> 21> 22> 23>		. (48	7)		ene =	PTR	206;	Acc	essi	on D	DBJ/	EMBL	/Gen	Bank	= 1	AF17	9731
	00> L Ala	175 Ile	Cys	His 5	Pro	Leu	His	Tyr	Ser 10	Thr	Ile	Met	Ala	Leu 15	Arg			
Let	ı Cys	Ala	Ser 20	Leu	. Val	Ala	Ala	Pro 25	Trp	Val	Ile	Ala	Ile 30	Leu	Asn			
Pro	Leu	Leu 35	His	Thr	Leu	Met	Met 40	Ala	His	Leu	His	Phe 45	Cys	Ser	Asp			
Asn	Val 50	Ile	His	His	Phe	Phe 55	Cys	Asp	Ile	Asn	Ser 60	Leu	Leu	Pro	Leu			
Ser 65	Cys	Ser	Asn	Thr	Ser 70	Leu	Asn	Gln	Leu	Ser 75	Val	Leu	Ala	Thr	Val 80			
Gly	Leu	Ile	Phe	Val 85	Val	Pro	Ser	Val	Cys 90	Ile	Leu	Val	Ser	Tyr 95	Ile			
Leu	Ile	Val	Ser 100	Ala	Val	Met	Lys	Val 105	Pro	Ser	Ala	Gln	Gly 110	Lys	Leu			
Lys	Ala	Phe 115	Ser	Ile	Сув	Gly	Ser 120	His	Leu	Ala	Leu	Val 125	Ile	Leu	Phe			
Tyr	Gly 130	Ala	Ile	Thr	Gly	Val 135	Tyr	Met	Ser	Pro	Leu 140	Ser	Asn	His	Ser			
Thr 145	Glu	Lys	Asp	Ser	Ala 150	Ala	Ser	Val	Ile	Phe 155	Met	Val	Val	Ala	Pro 160			
Val	T 011																	

Val Leu

<210> 176 <211> 487

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t gtg gcg gtg tgt aac cct ctt ctc tac aca gtt gca atg tac cag agg
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  Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Tyr Gln Arg
ctt tgc tcc ttg ttg gtg gct aca tca tac tgt tgg ggg aga gtc tgt
                                                                             97
Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Cys Trp Gly Arg Val Cys
             2.0
tcc ctg aca ctt acc tac ttt cta ctg gaa tta tcc ttc aga gga aat
                                                                            145
Ser Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn
                                                                            193
aat atc att aat aac ttt gtc tgt gag cat gct gcc att gtt gct gtg
Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val
                                                60
tct tgc tct gac ccc tat gtg agc cag gag atc act tta gtt tct gcc Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala
                                                                            241
aca ttc aat gaa ata agc agc ctg gtg atc act ctc act tcc tat gct Thr Phe Asn Glu Ile Ser Ser Leu Val Ile Thr Leu Thr Ser Tyr Ala
                                                                            289
                 85
ttc att ttt atc act gtc atg aag acg gct tcc att ggg ggg cgc aag
                                                                            337
Phe Ile Phe Ile Thr Val Met Lys Thr Ala Ser Ile Gly Gly Arg Lys
                                   105
             100
aaa geg tte tte aeg tgt gee tee cae ttg aeg gee att ace att tte
                                                                            385
Lys Ala Phe Phe Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe
                               120
                                                                            433
cat ggg act att ctt ttc ctc tac tgt gtt cct aac tcc aaa agt tcg
His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Ser Ser
                          135
                                                140
tgg ctc atg gtc aag gtg gcc tct gtc ttt tac aca gtg gtc att ccc
                                                                            481
Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro
                                                                            487
atg ctg
Met Leu
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<213> Pan troglodytes
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<221> misc\_feature



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<222> (1)..(487)
<223> Taxon = 9598; gene = PTR207; Accession DDBJ/EMBL/GenBank = AF179732
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Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Tyr Gln Arg 1 5 10 15

Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Cys Trp Gly Arg Val Cys 20 25 30

Ser Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn 35 40 45

Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val 50 55 60

Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala 65 70 75 80

Thr Phe Asn Glu Ile Ser Ser Leu Val Ile Thr Leu Thr Ser Tyr Ala 85 90 95

Phe Ile Phe Ile Thr Val Met Lys Thr Ala Ser Ile Gly Gly Arg Lys
100 105 110

Lys Ala Phe Phe Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe 115 120 125

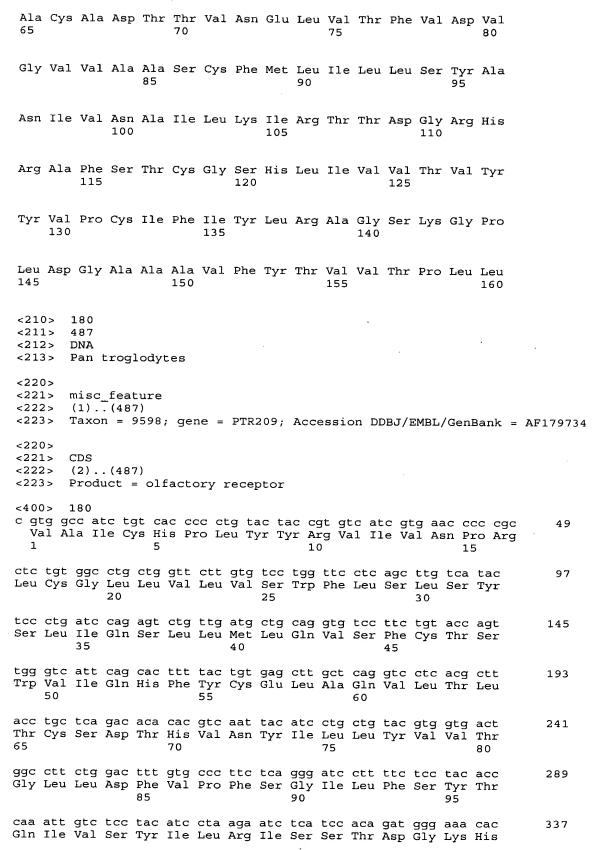
His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Ser Ser 130 135 140

Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro 145 150 155 160

- <210> 178
- <211> 481 <212> DNA
- <213> Pan troglodytes
- <220>
- <221> misc\_feature
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- <223> Taxon = 9598; gene = PTR208; Accession DDBJ/EMBL/GenBank = AF179733
- <220>
- <221> CDS
- <222> (2)..(481)
- <223> Product = olfactory receptor
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- c ctg gca ata tgt cag ccc ctg cgc tac cca gtg ctc atg aat ggg agg Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg

10 15 97 tta tgc aca gtc ctt gtg gct gga gct tgt gtc gcc ggc tcc atg cat Leu Cys Thr Val Leu Val Ala Gly Ala Cys Val Ala Gly Ser Met His ggg tct atc cag gcc acc ctg acc ttc cgc ctg ccc tac tgt ggg ccc Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro 145 aat cag gtg gat tac ttt atc tgt gac atc ccc gca gta ttg aga ctg 193 Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu 55 gcc tgt gct gac aca act gtc aat gag ctt gtg acc ttt gtg gac gtc Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Val 241 70 289 ggg gtg gtg gcc gcc agt tgc ttc atg tta att ctg ctc tcg tat gcc Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala 85 90 337 aac ata qta aat qcc atc ctq aaq ata cqc acc act qat qqq aqq cac Asn Ile Val Asn Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg His 385 egg gee tte tee ace tgt gge tee cae eta ate gtg gte aca gte tae Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr 120 tat gtc ccc tgt att ttc atc tac ctt agg gct ggc tcc aaa ggc ccc 433 Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Gly Pro ctg gat ggg gcg gct gtg ttt tac act gtt gtc act cca tta ctg 481 Leu Asp Gly Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu <210> 179 <211> 160 <212> PRT <213> Pan troglodytes <220> <221> misc\_feature <222> (1)..(481) Taxon = 9598; gene = PTR208; Accession DDBJ/EMBL/GenBank = AF179733 <223> Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg Leu Cys Thr Val Leu Val Ala Gly Ala Cys Val Ala Gly Ser Met His Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro

Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu



	100	105	5	110	
	e Ser Thr Cys		t ctg ttt gtg gtt s Leu Phe Val Val 125		85
			t agt tcc aat gca 1 Ser Ser Asn Ala 140		:33
			e atg tac act gtg l Met Tyr Thr Val 155	J	81
atg ctg Met Leu	·			4	:87
<210> 181 <211> 162 <212> PRT <213> Pan	troglodytes				
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Leu Cys Gly Leu Leu Val Leu Val Ser Trp Phe Leu Ser Leu Ser Tyr 20 25 30

Ser Leu Ile Gln Ser Leu Leu Met Leu Gln Val Ser Phe Cys Thr Ser 35 40 45

Trp Val Ile Gln His Phe Tyr Cys Glu Leu Ala Gln Val Leu Thr Leu 50 55 60

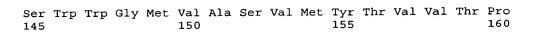
Thr Cys Ser Asp Thr His Val Asn Tyr Ile Leu Leu Tyr Val Val Thr 65 70 75 80

Gly Leu Leu Asp Phe Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr 85 90 95

Gln Ile Val Ser Tyr Ile Leu Arg Ile Ser Ser Thr Asp Gly Lys His 100 \$105\$

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Phe Val Val Ser Leu Phe 115 120 125

Tyr Gly Thr Gly Leu Gly Val Tyr Leu Ser Ser Asn Ala Ser Ser Ser 130 140



<210> 182 <211> 487 <212> DNA <213> Pan troglodytes	
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<220> <221> CDS <222> (2)(487) <223> Product = olfactory receptor	
<pre>&lt;400&gt; 182 t gta gcc ata tgt aat ccc ttg ctt tat cca gtg atg atg tcc aac aaa</pre>	19
ctc agc gct cag ttg cta agc att tca tat gta att ggt ttc ctg cat Leu Ser Ala Gln Leu Leu Ser Ile Ser Tyr Val Ile Gly Phe Leu His 20 25 30	97
cct ctg gtt cat gtg agt tta cta ttg cga cta act ttc tgc agg ttt Pro Leu Val His Val Ser Leu Leu Leu Arg Leu Thr Phe Cys Arg Phe 35 40 45	5
aac ata ata cat tat ttc tac tgt gaa att tta caa ctg ttc aaa att Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile 50 55 60	3
tca tgc aat ggt cca tct att aac gca cta atg ata ttt att ttt ggt Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Met Ile Phe Ile Phe Gly 65 70 75 80	1
gct ttt ata caa ata ccc act tta atg acg atc ata atc tct tat tct Ala Phe Ile Gln Ile Pro Thr Leu Met Thr Ile Ile Ile Ser Tyr Ser 85 90 95	39
cgt gtg ctc ttt gat att ctg aaa aaa aag tct gaa aag ggc aga agc Arg Val Leu Phe Asp Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser 100 105 110	37
aaa gcc ttc tcc aca tgc agc gcc cat ctg ctt tct gtc tca ttg tac Lys Ala Phe Ser Thr Cys Ser Ala His Leu Leu Ser Val Ser Leu Tyr 115 120 125	35
tac gga act ctg atc ttc atg tat gtg cgt cct gca tct ggc tta gct Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala 130 135 140	33
gaa gac cca gac aaa gtg tat tct ctg ttt tac acg att ata att ccc Glu Asp Pro Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro 145 150 155 160	31
ctg cta Leu Leu	87

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Val Ala Ile Cys Asn Pro Leu Leu Tyr Pro Val Met Met Ser Asn Lys
Leu Ser Ala Gln Leu Leu Ser Ile Ser Tyr Val Ile Gly Phe Leu His
Pro Leu Val His Val Ser Leu Leu Leu Arg Leu Thr Phe Cys Arg Phe
Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile
Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Met Ile Phe Ile Phe Gly
Ala Phe Ile Gln Ile Pro Thr Leu Met Thr Ile Ile Ile Ser Tyr Ser
                                     90
Arg Val Leu Phe Asp Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser
                                 105
Lys Ala Phe Ser Thr Cys Ser Ala His Leu Leu Ser Val Ser Leu Tyr
        115
                            120
Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala
Glu Asp Pro Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro
                    150
Leu Leu
<210> 184
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<222> (1)...(487)

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<222>
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                                                                          49
  Val Ala Ile Cys His Pro Leu Arg Tyr Thr Val Leu Met Asn Ile His
                                       10
tte tge gge ttg etg att ett ete tee agg tte atg age act atg gat
                                                                          97
Phe Cys Gly Leu Leu Ile Leu Leu Ser Arg Phe Met Ser Thr Met Asp
                                 25
gcc ctg gtt cag agt ctg atg ata ttt cag ctg tcc ttc tgc aaa aac
                                                                         145
Ala Leu Val Gln Ser Leu Met Ile Phe Gln Leu Ser Phe Cys Lys Asn
gtt gaa atc cct ttg ttc ttc tgt gaa gtc gtt cag gtc atc aag ctc Val Glu Ile Pro Leu Phe Phe Cys Glu Val Val Gln Val Ile Lys Leu
                                                                         193
gcc tgt tct gac acc ctc atc aac aac atc ctc ata tat ttt gca agt
                                                                         241
Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ser
                     70
age ata ttt ggt gea att eet ete tet gga ata att tte tet tat tet
                                                                         289
Ser Ile Phe Gly Ala Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ser
                85
                                      90
caa ata gtc acc tct gtt ctg aga atg cca tca gca aga gga aag tat
                                                                         337
Gln Ile Val Thr Ser Val Leu Arg Met Pro Ser Ala Arg Gly Lys Tyr
            100
aaa gcg ttt tcc acc tgt ggc tgt cac ctc tct gtt ttt tcc ttg ttc
                                                                         385
Lys Ala Phe Ser Thr Cys Gly Cys His Leu Ser Val Phe Ser Leu Phe
        115
tat ggg aca gct ttt ggg gtg tcc att agt tct gct gtt gct gag tct
                                                                         433
Tyr Gly Thr Ala Phe Gly Val Ser Ile Ser Ser Ala Val Ala Glu Ser
tcc cga att act gct gtg ggt tca gtg atg tac act gtg gtc cca caa
                                                                         481
Ser Arg Ile Thr Ala Val Gly Ser Val Met Tyr Thr Val Val Pro Gln
                     150
                                          155
                                                                         487
atg atg
Met Met
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Val Ala Ile Cys His Pro Leu Arg Tyr Thr Val Leu Met Asn Ile His
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Phe Cys Gly Leu Leu Ile Leu Leu Ser Arg Phe Met Ser Thr Met Asp
Ala Leu Val Gln Ser Leu Met Ile Phe Gln Leu Ser Phe Cys Lys Asn
        35
                            40
Val Glu Ile Pro Leu Phe Phe Cys Glu Val Val Gln Val Ile Lys Leu
Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ser
                    70
Ser Ile Phe Gly Ala Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ser
Gln Ile Val Thr Ser Val Leu Arg Met Pro Ser Ala Arg Gly Lys Tyr
Lys Ala Phe Ser Thr Cys Gly Cys His Leu Ser Val Phe Ser Leu Phe
        115
                            120
Tyr Gly Thr Ala Phe Gly Val Ser Ile Ser Ser Ala Val Ala Glu Ser
Ser Arg Ile Thr Ala Val Gly Ser Val Met Tyr Thr Val Val Pro Gln
                    150
Met Met
<210> 186
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                                                                      49
  Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
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97

ctc tgt gtc ttc tta gtg gct gta tct tgg att ctg tct tgt gcc agc

Leu Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser

Ser	Leu	Ser 35	His	Thr	Leu	Leu	Leu 40	Thr	Arg	Leu	Ser	Phe 45	Cys	Ala	Ala	142	,
aac Asn	acc Thr 50	atc Ile	ccc Pro	cat His	gtc Val	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	gct Ala	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ctg Leu	193	•
tcc Ser 65	tgc Cys	tca Ser	gat Asp	atc Ile	ttc Phe 70	ctc Leu	aat Asn	gag Glu	ctg Leu	gtc Val 75	atg Met	ttc Phe	aca Thr	gta Val	80 GJÀ āāā	241	
gtg Val	gtg Val	gtc Val	att Ile	acc Thr 85	ctg Leu	cca Pro	ttc Phe	atg Met	tgt Cys 90	atc Ile	ctg Leu	gta Val	tca Ser	tat Tyr 95	ggc Gly	289	
			gcc Ala 100													337	
aaa Lys	gca Ala	ttg Leu 115	tcc Ser	aca Thr	tgt Cys	ggc Gly	tcc Ser 120	cat His	ctc Leu	tct Ser	gtg Val	gtg Val 125	tct Ser	ctc Leu	tat Tyr	385	
tat Tyr	999 Gly 130	tca Ser	ata Ile	ttt Phe	ggc Gly	cag Gln 135	tac Tyr	ctt Leu	ttc Phe	ccg Pro	act Thr 140	gta Val	agc Ser	agt Ser	tct Ser	433	
att Ile 145	gac Asp	aag Lys	gat Asp	gtc Val	att Ile 150	gtg Val	gct Ala	ctc Leu	atg Met	tac Tyr 155	acg Thr	gtg Val	gtc Val	aca Thr	ccc Pro 160	481	
atg Met	_															487	
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<400 Val 1		.87 Ile	Cys	His 5	Pro	Leu	His	Tyr	Thr 10	Val	Ile	Met	Arg	Glu 15	Glu		
Leu	Cys	Val	Phe 20	Leu	Val	Ala	Val	Ser 25	Trp	Ile	Leu	Ser	Cys 30	Ala	Ser		
Ser	Leu	Ser 35	His	Thr	Leu	Leu	Leu 40	Thr	Arg	Leu	Ser	Phe 45	Сув	Ala	Ala		
Asn	Thr 50	Ile	Pro	His	Val	Phe 55	Сув	Asp	Leu	Ala	Ala 60	Leu	Leu	Lys	Leu		
Ser 65	Cys	Ser	Asp	Ile	Phe 70	Leu	Asn	Glu	Leu	Val 75	Met	Phe	Thr	Val	Gly 80		

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Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
            100
                                105
                                                    110
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
        115
                            120
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser
                        135
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
                                        155
Met Leu
<210>
      188
<211>
      484
<212>
      DNA
<213> Hylobates lar
<220>
<221>
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<222>
      (1) . . (484)
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= AF179738
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                                                                      60
gatggcagca ctgagctggg ggacaggctt tgccaactca ctgctacagt ccatccttgt
                                                                     120
ctggcgcctc cctttctgtg gccacaacgt catcaaccac tttttctgtg agatcttggc
                                                                     180
agtgctaaaa ctggcctgtg gggacatctc cctcaatgcg ctggcattaa tggtggccac
                                                                     240
agetyteety acaetygeee ecetettyet catetycety tettacettt teatettyte
                                                                     300
tgccatcctt agggtaccct ctgctgcagg ccggcgcaaa gccttctcca cctgctcagc
                                                                     360
ccacctcaca gtggtggtgg ttttttaagg gacaatttcc ttcatgtact tcaaacccaa
                                                                     420
ggccaaggac cccaacgtgg ataagattgt tgcattgttg tatggggttg tgacaccctc
                                                                     480
gctg
                                                                     484
<210>
      189
<211>
      487
<212>
      DNA
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<sup>&</sup>lt;220>

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<sup>&</sup>lt;223> Taxon = 9580; gene = HLA122; Accession DDBJ/EMBL/GenBank = AF179739

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<222> (2)..(487)
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                                                                           49
   Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg
                                         10
 ctt tgc tcc ttg ttg gtg gct aca tca tac tct tgg ggg ata gtc tgt
                                                                           97
 Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Ser Trp Gly Ile Val Cys
             20
                                   25
 ttc ctg aca ctt acc tac ttt cta ctg gaa tta tcc ttc aga gga aat
                                                                          145
 Phe Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn
 aat atc att aat aac ttt gtc tgt gag cat gct gcc att gtt gct gtg
                                                                          193
 Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val
     50
 tet tge tet gae eee tat gtg age cag gag ate act tta gtt tet gee
                                                                          241
 Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala
aca tto aat gaa ata ago agt otg atg att tto act too tat got
                                                                          289
Thr Phe Asn Glu Ile Ser Ser Leu Met Met Ile Phe Thr Ser Tyr Ala
                                      90
ttc att ttt atc act gtc atg aag atg cct tcc act ggg ggg cgc aag
                                                                         337
Phe Ile Phe Ile Thr Val Met Lys Met Pro Ser Thr Gly Gly Arg Lys
                                  105
aaa gcg ttc tcc acg tgt gcc tcc cac ctg acc gcc att acc att ttc
                                                                         385
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe
        115
cat ggg act atc ctt ttc ccc tac tgt gtt cct aac tcc aaa agt tca
His Gly Thr Ile Leu Phe Pro Tyr Cys Val Pro Asn Ser Lys Ser Ser
tgg ctc atg gtc aag gtg acc tct gtc ttt tac aca gtg ttc att ccc Trp Leu Met Val Lys Val Thr Ser Val Phe Tyr Thr Val Phe Ile Pro
                                                                         481
                     150
                                          155
atg gtg
                                                                         487
Met Val
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<400> 190
Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg
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Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Ser Trp Gly Ile Val Cys
                                 25
 Phe Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn
 Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val
 Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala
Thr Phe Asn Glu Ile Ser Ser Leu Met Met Ile Phe Thr Ser Tyr Ala
                                     90
Phe Ile Phe Ile Thr Val Met Lys Met Pro Ser Thr Gly Gly Arg Lys
             100
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe
        115
His Gly Thr Ile Leu Phe Pro Tyr Cys Val Pro Asn Ser Lys Ser Ser
                         135
Trp Leu Met Val Lys Val Thr Ser Val Phe Tyr Thr Val Phe Ile Pro
Met Val
<210> 191
<211> 486
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      (2)..(484)
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<400> 191
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                                                                        49
 Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
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cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt 97
Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
20 25 30

gct ctt ttg cat acc ctc ctc ctg gcc cag ctt tcc ttt tgt gct gac 145 Ala Leu Leu His Thr Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp

Cac atc ggg gtc acc atc ctc cag atc ctc ggt ggg gtc acc atc ggg ggg gtg leu ggg ggg ggg ggg leu ggg ggg leu ggg ggg leu ggg ggg ggg leu ggg ggg ggg ggg ggg ggg ggg ggg ggg g	
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 80  ttg aca gcc att atg ctt cca ttc ttg tgc atc ctg gtt tct tat ggt Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 95  cac att ggg gtc acc atc ctc cag att ccc tct acc aag ggc ata tgc His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys 110  aaa gcc ttg tcc act tgt gga tcc cac ctc tca gtg gtg act atc tat Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 115  tat ggg aca att att ggt ctc tat ttt ctt ctc ccc cag acc acc Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr 130  aat gac aag aac att att gct tca gtg ata tac aca gta gtc act ccc Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 145	193
Leu Thr Ala Ile Met Beu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 90 Cac att ggg gtc acc atc ctc cag att ccc tct acc aag ggc ata tgc His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys 110	241
His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys 110   aaa gcc ttg tcc act tgt gga tcc cac ctc tca gtg gtg act atc tat Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 115   tat ggg aca att att ggt ctc tat ttt ctt ccc cca tcc agc aac acc Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr 130   aat gac aag aac att att gct tca gtg ata tac aca gta gtc act ccc Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 145	289
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 115	337
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr 130 135 140  aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 145 150 150 160	385
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 145 150 155 160	433
ato tt	481
atg tt Met	486
<210> 192 <211> 161 <212> PRT <213> Hylobates lar	
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<pre>&lt;400&gt; 192 Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser 1</pre>	
Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys 20 25 30	
Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp 35 40 45	
His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 50 55 60	

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 85 90 95	
His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys 100 105 110	
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 115 120 125	
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr 130 135 140	
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 145 150 155 160	
Met	
<210> 193 <211> 487 <212> DNA <213> Hylobates lar	
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, , , , , , , , , , , , , , , , , , , ,	F I / J / 4 I
<pre>&lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (2)(487) &lt;223&gt; Product = olfactory receptor</pre>	F1/9/41
<220> <221> CDS <222> (2)(487)	49
<pre>&lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (2)(487) &lt;223&gt; Product = olfactory receptor &lt;400&gt; 193 t gtg gcc atc tgt agt ccc ttg cac tac cca gtc atc atg aac caa agg Val Ala Ile Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg</pre>	
<pre>&lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (2)(487) &lt;223&gt; Product = olfactory receptor  &lt;400&gt; 193 t gtg gcc atc tgt agt ccc ttg cac tac cca gtc atc atg aac caa agg    Val Ala Ile Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg    1</pre>	49
<pre> &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (2)(487) &lt;223&gt; Product = olfactory receptor  &lt;400&gt; 193 t gtg gcc atc tgt agt ccc ttg cac tac cca gtc atc atg aac caa agg   Val Ala Ile Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg   1</pre>	49 97
<pre> &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (2)(487) &lt;223&gt; Product = olfactory receptor  &lt;400&gt; 193 t gtg gcc atc tgt agt ccc ttg cac tac cca gtc atc atg aac caa agg    Val Ala Ile Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg    1</pre>	49 97 145
<pre> &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (2)(487) &lt;223&gt; Product = olfactory receptor  &lt;400&gt; 193 t gtg gcc atc tgt agt ccc ttg cac tac cca gtc atc atg aac caa agg     Val Ala Ile Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg     1</pre>	49 97 145

aaa Lys	gcc Ala	ttc Phe 115	tct Ser	acg Thr	tgt Cys	tcc Ser	tca Ser 120	cac His	ctc Leu	ctt Leu	gtt Val	gtc Val 125	tct Ser	ctt Leu	ttc Phe	385
tat Tyr	ata Ile 130	tca Ser	tta Leu	agc Ser	ctc Leu	aca Thr 135	tat Tyr	ttt Phe	cgg Arg	cct Pro	aaa Lys 140	tca Ser	aat Asn	aat Asn	tct Ser	433
cct Pro 145	gag Glu	ggc Gly	aag Lys	aag Lys	ctg Leu 150	cta Leu	tca Ser	ttg Leu	tcc Ser	tac Tyr 155	act Thr	gtt Val	gtg Val	act Thr	ccc Pro 160	481
atg Met	_															487

<210> 194 <211> 162 <212> PRT

<213> Hylobates lar

<220>

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<222> (1)..(487)

<223> Taxon = 9580; gene = HLA124; Accession DDBJ/EMBL/GenBank = AF179741

<400> 194

Val Ala Ile Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg

Thr Arg Ala Lys Leu Ala Ala Ser Trp Phe Pro Gly Phe Pro Val

Ala Thr Val Gln Thr Thr Trp Leu Phe Ser Phe Pro Phe Cys Gly Thr

Asn Lys Val Asn His Phe Phe Cys Asp Ser Pro Pro Val Leu Arg Leu 50 55

Val Cys Ala Asp Thr Ala Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr

Ile Leu Val Val Met Ile Pro Cys Leu Leu Ile Leu Cys Ser Tyr Thr

His Ile Ala Ala Ala Ile Leu Lys Ile Pro Ser Ala Lys Gly Lys Asn 105

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe

Tyr Ile Ser Leu Ser Leu Thr Tyr Phe Arg Pro Lys Ser Asn Asn Ser 130 135 140

## Pro Glu Gly Lys Lys Leu Leu Ser Leu Ser Tyr Thr Val Val Thr Pro 145 150 155 160

<210> 195 <211> 487 <212> DNA <213> Hylobates lar	
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gtc tgc ata ctg ctt gtt ttt act tct tgg ctg att tca ttc tta atc Val Cys Ile Leu Leu Val Phe Thr Ser Trp Leu Ile Ser Phe Leu Ile 20 25 30	97
ata ttc cct gca ctc atg ttg ctc tta aag ctt gat tac tgt agg tct Ile Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Arg Ser 35 40 45	145
aat att att gac cat ttt acc tgt gat tat ttt ccc ctg ctg caa ctt Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu 50 55 60	193
gct tgt tca gac aca aaa ttc tta gag gtg atg gca ttt tct tgt gct Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Ala Phe Ser Cys Ala 65 70 75 80	241
gtg ttt act cta atg ttc act ttg gca tta ata tct ctg tcc tac ata Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Ser Leu Ser Tyr Ile 85 90 95	289
tac att atc aga aca att ttg aga att cct tct act agt cag agg aca Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr 100 105 110	337
aag gcc ttt tcc aca tgt tct tcc cac atg gtt gtt att tcc atc tct Lys Ala Phe Ser Thr Cys Ser Ser His Met Val Val Ile Ser Ile Ser 115 120 125	385
tat ggc agc tgc att ttt atg tac att aaa ccc tca gca aaa gat aga Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg 130 135 140	433
gtg tcc ttg agc aag gga gtg gca ata cta aac acc tca gta gcc ccc Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Ala Pro 145 150 155 160	481
atg atg Met Met	487

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<210> 196
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<212> PRT
<213> Hylobates lar
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Val Ala Ile Cys Lys Pro Leu His Tyr Leu Asn Ile Met Asn Arg Arg
Val Cys Ile Leu Leu Val Phe Thr Ser Trp Leu Ile Ser Phe Leu Ile
Ile Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Arg Ser
Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Ala Phe Ser Cys Ala
Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Ser Leu Ser Tyr Ile
                                     90
Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr
            100
                                 105
Lys Ala Phe Ser Thr Cys Ser Ser His Met Val Val Ile Ser Ile Ser
        115
                             120
                                                  125
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Ala Pro
Met Met
<210> 197
<211> 484
<212> DNA
<213> Hylobates lar
<220>
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       (2)..(484)
<222>
       Product = olfactory receptor
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                                                                         49
  Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
ctc tgt gtc ttc tta gtg gct ata tct tgg att ctg tct tgt gcc agc
                                                                         97
Leu Cys Val Phe Leu Val Ala Ile Ser Trp Ile Leu Ser Cys Ala Ser
tcc ctc tct cac acc ctt ctc ctg acc cgg ctg tct ttc tgt gct gcg
                                                                        145
Ser Leu Ser His Thr Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
        35
                             40
aac acc atc ccc cac gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg
                                                                        193
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
                                                                        241
                                                                        289
gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
                                     90
                85
tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac
                                                                        337
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
            100
                                 105
aaa geg tee aeg tgt gge tee cat ett tet gtg gtg tet ete tat tat
                                                                        385
Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr
        115
                             120
ggg tca ata ttt ggc cag tac ctt ttc ccg acc gca agc agt tcc att
                                                                        433
Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile
gac aag gat gtc att gtg gct gtc atg tac aca gtg atc aca ccc atg
                                                                        481
Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met
                    150
                                         155
ttg
                                                                        484
Leu
<210> 198
<211> 161
<212> PRT
<213> Hylobates lar
<220>
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      misc_feature
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       Taxon = 9580; gene = HLA126; Accession DDBJ/EMBL/GenBank = AF179743
Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
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Leu Cys Val Phe Leu Val Ala Ile Ser Trp Ile Leu Ser Cys Ala Ser
Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
        35
                             40
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
                                 105
Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr
Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile
Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met
145
                    150
                                         155
Leu
<210> 199
<211> 487
<212> DNA
<213> Hylobates lar
<220>
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<223> Taxon = 9580; gene = HLA127; Accession DDBJ/EMBL/GenBank = AF179744
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<222> (2)..(487)
<223> Product = olfactory receptor
<400> 199
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                                                                       49
  Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
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cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys

25

gct ctt ttg cat acc ctc ctc ctg gcc cag ctt tcc ttt tgt gct gac 145 Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp 35 40 45	
cac atc atc cct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ttg 193 His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 50 55 60	
tcc tgc tca gat acc tcc ctc aat cag ttg gca atc ttt aca gca gga 241 Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 65 70 75 80	
ttg aca gcc att atg ctt cca ttc ttg tgc atc ctg gtt tct tat ggt 289 Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 85 90 95	
cac att ggg gtc acc atc ctc cag att ccc tct acc aag ggc ata tgc 337 His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys 100 105 110	
aaa gcc ttg tcc att tgt gga tcc cac ctc tca gtg gtg act atc tat 385 Lys Ala Leu Ser Ile Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 115 120 125	
tat ggg aca att att ggt ctc tat ttt ctt ccc cca tcc agc aac acc  Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr  130 135 140	
aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 145 150 155 160	
atg ttg Met Leu 487	
<210> 200 <211> 162 <212> PRT <213> Hylobates lar	
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<pre>&lt;400&gt; 200 Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser 1</pre>	
Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys 20 25 30	
Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp 35 40 45	
His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 50 55 60	
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 65 70 75 80	

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Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
                                90
His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
            100
                                105
                                                     110
Lys Ala Leu Ser Ile Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
                            120
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
                                        155
Met Leu
<210> 201
<211> 484
<212> DNA
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<220>
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       Taxon = 9580; gene = HLA128; Accession DDBJ/EMBL/GenBank = AF179745
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<223> Product = olfactory receptor
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                                                                       49
  Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
                                      10
ctc tgt gtc ttc tta gtg gct gta tct tgg att ctg tct tgt gcc agc
                                                                       97
Leu Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser
            20
                                25
tcc ctc tct cac acc ctt ctc ctg acc cgg ctg tct ttc tgt gct gcg
                                                                      145
Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
aac acc atc ccc cac gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg
                                                                      193
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
    50
tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg
                                                                      241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
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289

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly

tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac  Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His  100 105 110
aaa gcg tcc acg tgt ggc tcc cat ctt tct gtg gtg tct ctc tat tat  185  Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr  115  120  125
ggg tca ata ttt ggc cag tac ctt ttc ccg acc gca agc agt tcc att Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ile 130 135 140
gac aag gat gtc att gtg gct gtc atg tac aca gtg atc aca ccc atg Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met 145 150 155 160
ttg Leu
<210> 202 <211> 161 <212> PRT <213> Hylobates lar
<pre>&lt;220&gt; &lt;221&gt; misc_feature &lt;222&gt; (1)(484) &lt;223&gt; Taxon = 9580; gene = HLA128; Accession DDBJ/EMBL/GenBank AF179745</pre>
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Leu Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser 20 25 30
Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala 35 40 45
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80
Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His 100 105 110
Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr 115 120 125
Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile 130 135 140

Asp Lys Asp	var lie val Ala Val	Met Tyr Thr Val	Ile Thr Pro Met
145	150	155	160

Leu

<21 <21 <21 <21	1 > 2 >	203 484 DNA Hylo	bate	s la	r											
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<22 <22 <22 <22	1 > 2 >	CDS (2). Prod			fact	ory	rece	ptor								
<40 t g V	tg g	203 cc a la I	tc t le C	gt c ys H 5	ac c is P	ct c ro L	ta c eu H	at t is T	at g yr A 1	la T	cc a hr I	tc a le M	tg a et S	gt c er G 1	ag agc ln Ser 5	49
cag Gln	tgt Cys	gtc Val	atg Met 20	ctg Leu	gtg Val	gct Ala	ggg Gly	tcc Ser 25	tgg Trp	gtc Val	atc Ile	gct Ala	tgt Cys 30	gcg Ala	tgt Cys	97
gct Ala	ctt Leu	ttg Leu 35	cat His	acc Thr	ctc Leu	ctc Leu	ctg Leu 40	gcc Ala	cag Gln	ctt Leu	tcc Ser	ttt Phe 45	tgt Cys	gct Ala	gac Asp	145
cac His	atc Ile 50	atc Ile	cct Pro	cac His	ttc Phe	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	ggt Gly	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ttg Leu	193
tcc Ser 65	tgc Cys	tca Ser	gat Asp	acc Thr	ttc Phe 70	ctc Leu	aat Asn	gag Glu	ctg Leu	gtc Val 75	atg Met	ttc Phe	aca Thr	gta Val	80 GJA aaa	241
gtg Val	gtg Val	gtc Val	att Ile	acc Thr 85	ctg Leu	cca Pro	ttc Phe	atg Met	tgt Cys 90	atc Ile	ctg Leu	gta Val	tca Ser	tat Tyr 95	ggc Gly	289
tac Tyr	att Ile	Gly 999	gcc Ala 100	acc Thr	atc Ile	ctg Leu	agg Arg	gtc Val 105	cct Pro	tca Ser	acc Thr	aaa Lys	999 Gly 110	atc Ile	cac His	337
aaa Lys	gcg Ala	tcc Ser 115	acg Thr	tgt Cys	ggc Gly	tcc Ser	cat His 120	ctt Leu	tct Ser	gtg Val	gtg Val	tct Ser 125	ctc Leu	tat Tyr	tat Tyr	385
Gly aaa	tca Ser 130	ata Ile	ttt Phe	ggc	cag Gln	tac Tyr 135	ctt Leu	ttc Phe	ccg Pro	acc Thr	gca Ala 140	agc Ser	agt Ser	tcc Ser	att Ile	433
gac Asp 145	aag Lys	gat Asp	gtc Val	att Ile	gtg Val 150	gct Ala	gtc Val	atg Met	tac Tyr	aca Thr 155	gtg Val	atc Ile	aca Thr	ccc Pro	atg Met 160	481

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<210> 204
<211> 161
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<212> PRT

<213> Hylobates lar

<220>

<221> misc\_feature

<222> (1)..(484)

<223> Taxon = 9580; gene = HLA129; Accession DDBJ/EMBL/GenBank = AF179746

Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys

Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp 35 40

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 55

Ser Cys Ser Asp Thr Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly

Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His

Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr 115 120

Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ile

Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met 150

Leu

<210> 205

<211> 486

<212> DNA

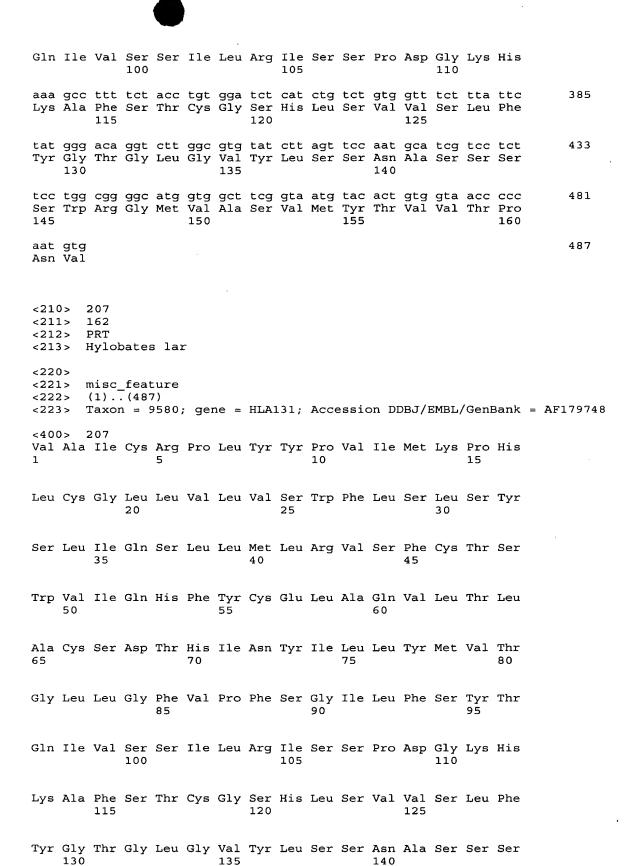
<213> Hylobates lar

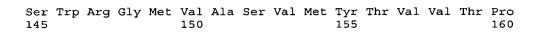
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= AF179747
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ctggtggctg ggtcctgggt catcgcttgt gcgtgtgctc ttttgcatac cctcctcctg
geocagettt cettttgtge tgaccacate atcecteact tettetgtga cettggtgee
                                                                      180
ctgctcaagt tgtcctgctc agatacctcc ctcaatcagt tggcaatctt tacagcagga
                                                                      240
ttgacageca ttatgettee attettgtge atcetggttt ettatggtea cattggggte
                                                                      300
accatectee agatteeete taccaaggge atatgeaaag eettgteeat ttgtggatee
                                                                      360
caceteteag tggtgactat ctattatggg acaattattg gtetetattt tetteececa
                                                                      420
tccagcaaca ccaatgacaa gaacataatt gcttcagtga tatacacagt agtcactccc
                                                                      480
atgttg
                                                                      486
<210>
       206
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       487
<212>
      DNA
<213>
      Hylobates lar
<220>
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<223>
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      CDS
<221>
<222>
       (2)..(487)
<223>
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<400> 206
t gtg gcc atc tgt cgc ccc ctg tac tac cct gtc atc atg aaa cct cac
                                                                       49
  Val Ala Ile Cys Arg Pro Leu Tyr Tyr Pro Val Ile Met Lys Pro His
                                      10
                                                           15
ctc tgt ggc ctg ctg gtt ctt gtg tcc tgg ttc ctc agc ttg tca tac
                                                                       97
Leu Cys Gly Leu Leu Val Leu Val Ser Trp Phe Leu Ser Leu Ser Tyr
            20
tee etg ate eag agt etg ttg atg etg egg gtg tee tte tge ace agt
                                                                      145
Ser Leu Ile Gln Ser Leu Leu Met Leu Arg Val Ser Phe Cys Thr Ser
tgg gtc att cag cac ttt tac tgt gag ctt gct cag gtc ctc acg ctt
                                                                      193
Trp Val Ile Gln His Phe Tyr Cys Glu Leu Ala Gln Val Leu Thr Leu
                        55
                                                                      241
gcc tgc tca gac aca cac atc aat tac atc ctg ctc tac atg gtg acc
Ala Cys Ser Asp Thr His Ile Asn Tyr Ile Leu Leu Tyr Met Val Thr
ggc ctt ttg ggc ttt gtg ccc ttc tca ggg atc ctt ttc tcc tac acc
                                                                      289
Gly Leu Leu Gly Phe Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr
                85
                                                         95
                                    90
```

337

caa atc gtc tcc tcc atc ctg aga atc tca tcc cca gat ggg aaa cac





Asn Val

<210> 208 <211> 487 <212> DNA <213> Hylobates lar	
<pre>&lt;221&gt; misc_feature &lt;222&gt; (1)(487) &lt;223&gt; Taxon = 9580; gene = HLA132; Accession DDBJ/EMBL/GenBa</pre>	ank = AF179749
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<pre>&lt;400&gt; 208 t gtg gcc atc tgt cac cct cta cat tat gcc acc atc atg agt cac Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Glr 1 5 10 15</pre>	
cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg t Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala C 20 25 30	gt 97 Cys
gct ctt ttg cat acc ctc ctc ctg gcc cag ctt tcc ttt tgt gct g Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala A 35 40 45	
cac atc atc cct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag t His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys I 50 55 60	
tcc tgc tca gat acc tcc ctc aat cag ttg gca atc ttt aca gca g Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala G 65 70 75 8	
ttg aca gcc att atg ctt cca ttc ttg tgc atc ctg gtt tct tat g Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr G 85 90 95	
cac att ggg gtc acc atc ctc cag act ccc tct acc aag ggc ata t His Ile Gly Val Thr Ile Leu Gln Thr Pro Ser Thr Lys Gly Ile C 100 105 110	
aaa gcc ttg tcc att tgt gga tcc cac ctc tca gtg gtg act atc t Lys Ala Leu Ser Ile Cys Gly Ser His Leu Ser Val Val Thr Ile T 115 120 125	
tat ggg aca att att ggt ctc tat ttt ctt ccc cca tcc agc aac a Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn T 130 135 140	
aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act c Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr F 145 150 155 1	
atg ttg	487

## Met Leu

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<210> 209
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<211> 162 <212> PRT

<213> Hylobates lar

<220>

<221> misc\_feature <222> (1)..(487)

<223> Taxon = 9580; gene = HLA132; Accession DDBJ/EMBL/GenBank = AF179749

<400> 209

Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser 5 10

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys

Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 90

His Ile Gly Val Thr Ile Leu Gln Thr Pro Ser Thr Lys Gly Ile Cys

Lys Ala Leu Ser Ile Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr 135

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 150 155

Met Leu

<210> 210

<211> 487 <212> DNA

<213> Gorilla gorilla

<220>

<221> misc\_feature

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<222>
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<223>
       Taxon = 9593; gene = GGO100; Accession DDBJ/EMBL/GenBank = AF179750
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      CDS
<221>
<222>
       (2)..(487)
<223>
      Product = olfactory receptor
<400> 210
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                                                                       49
  Val Ala Ile Cys His Pro Leu His Tyr Thr Phe Ile Met Asp Gln Asn
                                       10
ace tge att caa etg gea gtt att tet tgg tee agt age tte etg tgt
                                                                       97
Thr Cys Ile Gln Leu Ala Val Ile Ser Trp Ser Ser Ser Phe Leu Cys
                                 25
tcc atg gtt atc aat gtt ctc acg ttg agt ttg ccc tac tgt ggg cct
                                                                      145
Ser Met Val Ile Asn Val Leu Thr Leu Ser Leu Pro Tyr Cys Gly Pro
                            40
aat atc ctg aat cac ttt ttc tgt gag gta cct act gtc ctg agg ttg
                                                                      193
Asn Ile Leu Asn His Phe Phe Cys Glu Val Pro Thr Val Leu Arg Leu
tet tge ace gae ace tea tte acg gag etg gtt gtt ttt ate tte agt
                                                                      241
Ser Cys Thr Asp Thr Ser Phe Thr Glu Leu Val Val Phe Ile Phe Ser
                    70
ate ate att gte tte ate eet tte ete ete att gtt gtt tee tat gte
                                                                      289
Ile Ile Ile Val Phe Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val
                                    90
cgg atc ctt caa tct gtt ctc agg atg cgg tca gcc tcc ggg cgg tat
                                                                      337
Arg Ile Leu Gln Ser Val Leu Arg Met Arg Ser Ala Ser Gly Arg Tyr
                                                     110
aag gca tta tcc acc tgt acc tcc cat ttg aca gtg gta acc tta ttt
                                                                      385
Lys Ala Leu Ser Thr Cys Thr Ser His Leu Thr Val Val Thr Leu Phe
        115
                            120
tat ggg act gcc atc ctc atg tac atg aga cca cag tcg agg tct tcc
                                                                      433
Tyr Gly Thr Ala Ile Leu Met Tyr Met Arg Pro Gln Ser Arg Ser Ser
    130
                        135
tgg gct ggc ggc aag atc att gcg gtt ttc tac acg gtg gtc aca ccc
                                                                      481
Trp Ala Gly Gly Lys Ile Ile Ala Val Phe Tyr Thr Val Val Thr Pro
145
                    150
atg ctt
                                                                      487
Met Leu
<210>
       211
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       162
<212>
       PRT
<213>
      Gorilla gorilla
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<222>
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      Taxon = 9593; gene = GGO100; Accession DDBJ/EMBL/GenBank = AF179750
<400> 211
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Val Ala Ile Cys His Pro Leu His Tyr Thr Phe Ile Met Asp Gln Asn

15

Thr	Сув	Ile	Gln 20		Val		-			Leu	Сув

10

Ser Met Val Ile Asn Val Leu Thr Leu Ser Leu Pro Tyr Cys Gly Pro 40 45

Asn Ile Leu Asn His Phe Phe Cys Glu Val Pro Thr Val Leu Arg Leu

Ser Cys Thr Asp Thr Ser Phe Thr Glu Leu Val Val Phe Ile Phe Ser 70

Ile Ile Ile Val Phe Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val 90 85

Arg Ile Leu Gln Ser Val Leu Arg Met Arg Ser Ala Ser Gly Arg Tyr 105

Lys Ala Leu Ser Thr Cys Thr Ser His Leu Thr Val Val Thr Leu Phe

Tyr Gly Thr Ala Ile Leu Met Tyr Met Arg Pro Gln Ser Arg Ser Ser 130 135

Trp Ala Gly Gly Lys Ile Ile Ala Val Phe Tyr Thr Val Val Thr Pro 155

Met Leu

<210> 212 <211> 488 <212> DNA

<213> Gorilla gorilla

<220>

<221> misc\_feature

<222> (1). (488) <223> Taxon = 9593; gene = GGO101; pseudogene; Accession DDBJ/EMBL/GenBank = AF179751

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C	ccacc	tgac	agc	tgtc	acc	ctct	tcta	tg g	ggca	gcca	t gt	tcat	ctac	ctg	aggccta	a 420
gg	geget	accg	ggc	cccc	agc	catg	acaa	gg t	ggcc	tcta	t ct	tcta	caca	gtc	cttacto	2 480
C	catgo	tg														488
<2 <2	210> 211> 212> 213>	213 487 DNA Gor		gor:	illa											
<2 <2	20> 21> 22> 23>	(1)	(4			ene =	= GG(	0102	; Acc	cessi	on I	DBJ,	⁄емві	L/Ger	nBank =	- AF179752
<2 <2	20> 21> 22> 23>		(48 duct	37) = 01	fact	ory	rece	eptor	c c							
t	gtt g	213 tc a al ]	ata t [le (	gt c Ys H	lıs F	ct c ro L	tc c eu H	ac t Iis T	yr I	ict g hr V	tc a al I	itc a :le M	itg a Iet A	rg G	gaa gag Glu Glu .5	49
tt Ph	c tgt e Cys	gto Val	tto Phe 20	tta Leu	gtg Val	gct Ala	gta Val	tct Ser 25	tgg Trp	att Ile	ctg Leu	tct Ser	tgt Cys 30	gcc Ala	agc Ser	97
tc: Se:	c ctc r Leu	tct Ser 35	cac His	acc Thr	gtt Val	ctc Leu	ctg Leu 40	acc Thr	cag Gln	ctg Leu	tct Ser	ttc Phe 45	tgt Cys	gct Ala	gcg Ala	145
aad Asr	acc Thr 50	atc Ile	ccc	cat His	gtc Val	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	gct Ala	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ctg Leu	193
tco Ser 65	tgc Cys	tca Ser	gat Asp	atc Ile	ttc Phe 70	ctc Leu	aat Asn	gag Glu	ctg Leu	gtc Val 75	atg Met	ttc Phe	aca Thr	gta Val	80 Gly 333	241
gtç Val	gtg Val	gtc Val	att Ile	acc Thr 85	ctg Leu	cca Pro	ttc Phe	atg Met	tgt Cys 90	atc Ile	ctg Leu	gta Val	tca Ser	tat Tyr 95	ggt Gly	289
tac Tyr	att	Gly 999	gcc Ala 100	acc Thr	atc Ile	ctg Leu	Gly aaa	gtc Val 105	cct Pro	tca Ser	acc Thr	aaa Lys	999 Gly 110	atc Ile	cac His	337
aaa Lys	gca Ala	ttg Leu 115	tcc Ser	aca Thr	tgt Cys	ggc Gly	tcc Ser 120	cat His	ctc Leu	tct Ser	gtg Val	gtg Val 125	tct Ser	ctc Leu	tat Tyr	385
tat Tyr	999 Gly 130	tca Ser	ata Ile	ttt Phe	ggc Gly	cag Gln 135	tac Tyr	ctt Leu	ttc Phe	ccg Pro	act Thr 140	gta Val	agc Ser	agt Ser	ttt Phe	433
att [le	gac Asp	aag Lys	gat Asp	gtc Val	att Ile 150	gtg Val	gct Ala	ctc Leu	atg Met	tac Tyr 155	acg Thr	gtg Val	gtc Val	aca Thr	ccc Pro 160	481
icg	ttg															487

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<221> misc\_feature

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<210> 214
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<213> Gorilla gorilla
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<400> 214
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Phe Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser
            20
Ser Leu Ser His Thr Val Leu Leu Thr Gln Leu Ser Phe Cys Ala Ala
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
                                    90
Tyr Ile Gly Ala Thr Ile Leu Gly Val Pro Ser Thr Lys Gly Ile His
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Phe
                        135
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
                    150
                                        155
                                                             160
Thr Leu
<210> 215
<211>
      488
<212>
      DNA
<213> Gorilla gorilla
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<222> (1)..(488)
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= AF179753
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                                                                     60
gataaccatg ttgtcttggc tcctgggtgc agctgacggg ctcatgcagg ctgttgctac
                                                                     120
cctgagcttc ccatattgcg gtgcacacga gatcgatcac ttcttctgcg aggccccgt
                                                                     180
gctggttcat ttggcttgtg ctgacacttc agtcttcgaa aacgccatgt acatctgctg
                                                                     240
tgtgttaatg ctcctggtcc ccttttccct catcctgtcc tcctatggtc tcatcctcgc
                                                                     300
tgctgttctg cacatgcgct ctacagaagc ccgcaagaag gcctttgcca cctgctcttc
                                                                     360
acatttggct gtggtgggac tcttttatgg agctgccatt tttacctata tgagacccaa
                                                                     420
atcccacagg tccactaacc acgataaggt tgtgtcagcc ttctatagta tgttcacccc
                                                                     480
tttactaa
                                                                     488
<210> 216
<211>
      458
<212> DNA
<213> Gorilla gorilla
<220>
<221> misc_feature
<222> (1)..(458)
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= AF179754
<400> 216
ccaccatcat gagtcacage cagtgtgtca tgctggtggc tgggtcctgg gtcatcgctt
                                                                      60
gtgcgtgtgc tcttttgcat accetectec tggcccggct ttccttctgt gctgaccaca
                                                                     120
teatecetea ettettetgt gacettggtg ceetgeteaa gttgteetge teagacacet
                                                                     180
ccctcaatca gttagcaatc tttacagcag gattgacagc cattatgctt ccattcctgt
                                                                     240
gcatcctggt ttcttatggt cacattgggg tcaccatcct ccagattccc tctaccaagg
                                                                     300
gcatatgcaa agccttgtcc acttgtggat cccacctctc agtggtgact atctattatg
                                                                     360
ggacaattat tggtctctat tttcttcccc catcctgcaa caccaatgac gagaacataa
                                                                     420
                                                                     458
ttgcttcagt gatatacaca gtagtcactc ccatattg
<210> 217
<211>
      477
<212> DNA
<213> Gorilla gorilla
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<222> (2)..(475)

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 <400> 217
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                                                                          49
   Val Ala Ile Arg Lys Pro Leu His Tyr Leu Val Ile Met Arg Gln Trp
gtg tgt gtt gtg ctg ctg gta atg tcc tgg gtt gga gga ttt ctg cac Val Cys Val Val Leu Leu Val Met Ser Trp Val Gly Gly Phe Leu His
                                                                          97
             20
 tca gta ttt caa ctt agc att att tat ggg ctc cca ttc tgt ggc ccc
                                                                         145
Ser Val Phe Gln Leu Ser Ile Ile Tyr Gly Leu Pro Phe Cys Gly Pro
aat gtc att gat cac ttt ttc tgt gac atg tat ccc tta ttg aaa ctg
                                                                         193
Asn Val Ile Asp His Phe Phe Cys Asp Met Tyr Pro Leu Leu Lys Leu
                         55
gtc tgc act gac acc cat gtt att ggc ctc tta gtg gtg acc aat gga
                                                                         241
Val Cys Thr Asp Thr His Val Ile Gly Leu Leu Val Val Thr Asn Gly
                     70
gga ctg tct tgc act att gtg ttt ctg ctc tta ctc atc tct tat ggt
                                                                         289
Gly Leu Ser Cys Thr Ile Val Phe Leu Leu Leu Leu Ile Ser Tyr Gly
                 85
gtc atc ttg cac tct cta aag aaa ctt agt cag aaa ggg agg caa aaa
                                                                         337
Val Ile Leu His Ser Leu Lys Lys Leu Ser Gln Lys Gly Arg Gln Lys
             100
ged etc tea acc tge agt tee eac atc act gtg gtt gte tte ttt
                                                                         385
Ala Leu Ser Thr Cys Ser Ser His Ile Thr Val Val Val Phe Phe
gtt cct tgt att ttt atg tat gct aga cct gct agg agc ttc ccc att
                                                                         433
Val Pro Cys Ile Phe Met Tyr Ala Arg Pro Ala Arg Ser Phe Pro Ile
                         135
gac aaa tca gtg agt gtg ttt tat aca gtc ata acc cca atg ct
                                                                        477
Asp Lys Ser Val Ser Val Phe Tyr Thr Val Ile Thr Pro Met
                     150
<210> 218
<211>
      158
<212>
       PRT
<213> Gorilla gorilla
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<221>
      misc_feature
<222>
       (1)..(477)
       Taxon = 9593; gene = GGO106; Accession DDBJ/EMBL/GenBank = AF179755
<400> 218
Val Ala Ile Arg Lys Pro Leu His Tyr Leu Val Ile Met Arg Gln Trp
Val Cys Val Val Leu Leu Val Met Ser Trp Val Gly Gly Phe Leu His
            20
                                 25
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Ser Val Phe Gln Leu Ser Ile Ile Tyr Gly Leu Pro Phe Cys Gly Pro

40

35

Asn	Val 50	Ile	Asp	His	Phe	Phe 55	Cys	Asp	Met	Tyr	Pro 60	Leu	Leu	Lys	Leu	
Val 65	Cys	Thr	Asp	Thr	His 70	Val	Ile	Gly	Leu	Leu 75	Val	Val	Thr	Asn	Gly 80	
Gly	Leu	Ser	Cys	Thr 85	Ile	Val	Phe	Leu	Leu 90	Leu	Leu	Ile	Ser	Tyr 95	Gly	
Val	Ile	Leu	His 100	Ser	Leu	Lys	Lys	Leu 105	Ser	Gln	Lys	Gly	Arg 110	Gln	Lys	
Ala	Leu	Ser 115	Thr	Cys	Ser	Ser	His 120	Ile	Thr	Val	Val	Val 125	Phe	Phe	Phe	
Val	Pro 130	Сув	Ile	Phe	Met	Tyr 135	Ala	Arg	Pro	Ala	Arg 140	Ser	Phe	Pro	Ile	
Asp 145	Lys	Ser	Val	Ser	Val 150	Phe	Tyr	Thr	Val	Ile 155	Thr	Pro	Met			
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					gcc Ala											145
					ttc Phe											193
gcc Ala 65	tgc Cys	acc Thr	aac Asn	aca Thr	cag Gln 70	gca Ala	gta Val	gag Glu	ctt Leu	gtg Val 75	gcc Ala	ttt Phe	gtg Val	att Ile	gct Ala 80	241

Val Val Val Ile Leu Ser Ser Cys Leu Ile Thr Leu Val Ser Tyr Val 85 90 95	
tac atc atc agc acc atc ctc agg atc ccc tct gcc agt ggc cgg agc  Tyr Ile Ile Ser Thr Ile Leu Arg Ile Pro Ser Ala Ser Gly Arg Ser  100 105 110	
aaa gcc ttc tcc acg tgc tcc tcg cat ctc acc gtg gtg ctc att tgg  Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp  115 120 125	
tat ggg tcc aca att ttc ctt cac gtc cgc acc tct atc aaa gac gcc Tyr Gly Ser Thr Ile Phe Leu His Val Arg Thr Ser Ile Lys Asp Ala 130 135 140	
ttg gat ctg atc aaa gct gtc cac gtc ctg aac act gtg gtg act cca Leu Asp Leu Ile Lys Ala Val His Val Leu Asn Thr Val Val Thr Pro 145 150 155 160	
gtt tta a Val Leu	
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Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp

115 120 125

Tyr Gly Ser Thr Ile Phe Leu His Val Arg Thr Ser Ile Lys Asp Ala 130 135 140

Leu Asp Leu Ile Lys Ala Val His Val Leu Asn Thr Val Val Thr Pro 145 150 150

Val Leu

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                                                                     120
gaattateet teagaggaaa taatateatt aataaetttg tetgtgagea egetgteatt
                                                                     180
gttgctgtgt cttgctctga cccctatttg agccaggaga tcactttagt ttctgccaac
                                                                     240
                                                                     300
attcaatgaa ataagcagcc tggtgatcat tctcacttcc tatgctttca tttttatcac
tgtcatgaag acgccttcca ctggggggcg caagaaagcg ttctccacgt gtgcctccca
                                                                     360
cttgacggcc attaccattt tccatgggac tatccttttc ctctactgtg ttcctaactc
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480

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<sup>&</sup>lt;210> 222

<sup>&</sup>lt;211> 487

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<sup>&</sup>lt;220>

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<sup>&</sup>lt;222> (1)..(487)

<sup>&</sup>lt;223> Taxon = 9593; gene = GGO109; Accession DDBJ/EMBL/GenBank = AF179758

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<sup>&</sup>lt;221> CDS

<sup>&</sup>lt;222> (2)..(487)

<sup>&</sup>lt;223> Product = olfactory receptor

<sup>&</sup>lt;400> 222

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Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser His Ser
1 5 10 15

cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt 97 Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys

			20					25					30	
gct Ala	ctt	ttg	cat Hie	acc	ctc	ctc	ctg	gcc	cgg	ctt	tcc	ttc	tgt	9

gct Ala	ctt Leu	ttg Leu 35	cat His	acc Thr	ctc Leu	ctc Leu	ctg Leu 40	gcc Ala	cgg Arg	ctt Leu	tcc Ser	ttc Phe 45	tgt Cys	gct Ala	gac Asp	145
cac His	atc Ile 50	atc Ile	cct Pro	cac His	ttc Phe	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	ggt Gly	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ttg Leu	193
tcc Ser 65	tgc Cys	tca Ser	gac Asp	acc Thr	tcc Ser 70	ctc Leu	aat Asn	cag Gln	tta Leu	gca Ala 75	atc Ile	ttt Phe	aca Thr	gca Ala	gga Gly 80	241
ttg Leu	aca Thr	gcc Ala	att Ile	atg Met 85	ctt Leu	cca Pro	ttc Phe	ctg Leu	tgc Cys 90	atc Ile	ctg Leu	gtt Val	tct Ser	tat Tyr 95	ggt Gly	289
cac His	att Ile	glå aaa	gtc Val 100	acc Thr	atc Ile	ctc Leu	cag Gln	att Ile 105	ccc Pro	tct Ser	acc Thr	aag Lys	ggc Gly 110	ata Ile	tgc Cys	337
aaa Lys	gcc Ala	ttg Leu 115	tcc Ser	act Thr	tgt Cys	gga Gly	tcc Ser 120	cac His	ctc Leu	tca Ser	gtg Val	gtg Val 125	act Thr	atc Ile	tat Tyr	385
tat Tyr	999 Gly 130	aca Thr	att Ile	att Ile	ggt Gly	ctc Leu 135	tat Tyr	ttt Phe	ctt Leu	ccc Pro	cca Pro 140	tcc Ser	agc Ser	aac Asn	acc Thr	433
aat Asn 145	gac Asp	aag Lys	aac Asn	ata Ile	att Ile 150	gct Ala	tca Ser	gtg Val	Ile	tac Tyr 155	aca Thr	gta Val	gtc Val	act Thr	ccc Pro 160	481
atg Met																487

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<400> 223

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Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys 20

Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp 35

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu

Ser 65	Cys	Ser	Asp	Thr	Ser 70	Leu	Asn	Gln	Leu	Ala 75	Ile	Phe	Thr	Ala	Gly 80	
Leu	Thr	Ala	Ile	Met 85	Leu	Pro	Phe	Leu	Сув 90	Ile	Leu	Val	Ser	Tyr 95	Gly	
His	Ile	Gly	Val 100	Thr	Ile	Leu	Gln	Ile 105	Pro	Ser	Thr	Lys	Gly 110	Ile	Cys	
Lys	Ala	Leu 115	Ser	Thr	Сув	Gly	Ser 120	His	Leu	Ser	Val	Val 125	Thr	Ile	Tyr	
Tyr	Gly 130	Thr	Ile	Ile	Gly	Leu 135	Tyr	Phe	Leu	Pro	Pro 140	Ser	Ser	Asn	Thr	
Asn 145	Asp	Lys	Asn	Ile	Ile 150	Ala	Ser	Val	Ile	Tyr 155	Thr	Val	Val	Thr	Pro 160	
Met	Leu															
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ctc Leu	agc Ser	gct Ala	cag Gln 20	ttg Leu	cta Leu	agt Ser	att Ile	tca Ser 25	tat Tyr	gta Val	att Ile	ggt Gly	ttc Phe 30	ctg Leu	cat His	97
cct	ctg Leu	gtt Val 35	cat His	gtg Val	agt Ser	tta Leu	cta Leu 40	ttg Leu	cga Arg	cta Leu	act Thr	ttc Phe 45	tgc Cys	agg Arg	ttt Phe	145
aac Asr	ata Ile	ata : Ile	cat His	tat Tyr	ttc Phe	tac Tyr 55	tgt Cys	gaa Glu	att Ile	tta Leu	caa Gln 60	ctg Leu	ttc Phe	aaa Lys	att Ile	193
tca Ser 65	tgc Cys	aat Asn	ggt Gly	cca Pro	tct Ser 70	att Ile	aac Asn	gca Ala	cta Leu	ata Ile 75	ata Ile	ttt Phe	att Ile	ttt Phe	ggt Gly 80	241
act		ata	саа	ata	ccc	act	tta	atq	act	ato	ata	atc	tct	tat	act	289

Ala	Phe	Ile	Gln	Ile 85	Pro	Thr	Leu	Met	Thr 90	Ile	Ile	Ile	Ser	Tyr 95	Thr	
cgt Arg	gtg Val	ctc Leu	ttt Phe 100	gat Asp	att Ile	ctg Leu	aaa Lys	aaa Lys 105	aag Lys	tct Ser	gaa Glu	aag Lys	ggc Gly 110	aga Arg	agc Ser	337
aaa Lys	gcc Ala	ttc Phe 115	tcc Ser	aca Thr	tgc Cys	ggc Gly	gcc Ala 120	cat His	ctg Leu	ctt Leu	tct Ser	gtc Val 125	tca Ser	ttg Leu	tac Tyr	385
tac Tyr	gga Gly 130	act Thr	ctg Leu	atc Ile	ttc Phe	atg Met 135	tat Tyr	gtg Val	cgt Arg	cct Pro	gca Ala 140	tct Ser	ggc Gly	tta Leu	gct Ala	433
gaa Glu 145	gac Asp	caa Gln	gac Asp	aaa Lys	gtg Val 150	tat Tyr	tct Ser	ctg Leu	ttt Phe	tac Tyr 155	acg Thr	att Ile	ata Ile	att Ile	ccc Pro 160	481
_	cta Leu															487
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Val 1		Ile		5					10					15		·
Val 1 Leu	Ala	Ile Ala	Gln 20	5 Leu	Leu	Ser	Ile	Ser 25	10 Tyr	Val	Ile	Gly	Phe 30	15 Leu	His	·
Val 1 Leu	Ala	Ile Ala Val	Gln 20 His	5 Leu Val	Leu Ser	Ser	Ile Leu 40	Ser 25 Leu	10 Tyr Arg	Val Leu	Ile Thr	Gly Phe 45	Phe 30 Cys	15 Leu Arg	His Phe	
Val 1 Leu Pro	Ala Ser Leu	Ile Ala Val 35	Gln 20 His	5 Leu Val Tyr	Leu Ser Phe	Ser Leu Tyr 55	Ile Leu 40	Ser 25 Leu Glu	Tyr Arg	Val Leu Leu	Ile Thr Gln	Gly Phe 45	Phe 30 Cys	Leu Arg	His Phe Ile	
Val 1 Leu Pro Asn Ser 65	Ala Ser Leu	Ile Ala Val 35 Ile Asn	Gln 20 His His	5 Leu Val Tyr Pro	Leu Ser Phe Ser 70	Ser Leu Tyr 55	Ile Leu 40 Cys	Ser 25 Leu Glu Ala	Tyr Arg Ile	Val Leu Leu Ile 75	Ile Thr Gln 60 Ile	Gly Phe 45 Leu Phe	Phe 30 Cys Phe	Lys Phe	His Phe Ile Gly	
Val 1 Leu Pro Asn Ser 65	Ala Ser Leu Ile 50 Cys	Ile Ala Val 35 Ile Asn	Gln 20 His Gly	5 Leu Val Tyr Pro	Leu Ser Phe Ser 70	Ser Leu Tyr 55 Ile	Ile Leu 40 Cys Asn	Ser 25 Leu Glu Ala Met	Tyr Arg Ile Leu Thr	Val Leu Leu Ile 75	Ile Thr Gln 60 Ile	Gly Phe 45 Leu Phe	Phe 30 Cys Phe Ile	Leu Arg Lys Phe	His Phe Ile Gly 80 Thr	

Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala 130 135 140

Glu Asp Gln Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro 145 150 155 160

Leu Leu

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tcc ctc tct cac acc ctt ctc ctg acc cgg ctg tct ttc tgt gct gcg Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala 35 40 45
aac acc gtc ccc cat gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg Asn Thr Val Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60
tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 70 75 80
gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95
tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac  Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His  100 105 110
aaa gca ttg tcc aca tgt ggc tcc cat ctc tct gtg gtg tct ctc tat  185  Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr  115  120  125
tat ggg tca ata ttt ggc cag tac ctt ttc ccg act gta agc agt tct Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 130 135 140

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_	ttg Leu																487
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Leu	Cys	Val	Phe 20	Leu	Val	Ala	Val	Ser 25	Arg	Ile	Leu	Ser	Cys 30	Ala	Ser		
Ser	Leu	Ser 35	His	Thr	Leu	Leu	Leu 40	Thr	Arg	Leu	Ser	Phe 45	Суз	Ala	Ala		
Asn	Thr 50	Val	Pro	His	Val	Phe 55	Сув	Asp	Leu	Ala	Ala 60	Leu	Leu	Lys	Leu		
Ser 65	Cys	Ser	Asp	Ile	Phe 70	Leu	Asn	Glu	Leu	Val 75	Met	Phe	Thr	Val	Gly 80		
Val	Val	Val	Ile	Thr 85	Leu	Pro	Phe	Met	Cys 90	Ile	Leu	Val	Ser	Tyr 95	Gly		
Tyr	Ile	Gly	Ala 100	Thr	Ile	Leu	Arg	Val 105	Pro	Ser	Thr	Lys	Gly 110	Ile	His		
Lys	Ala	Leu 115	Ser	Thr	Сув	Gly	Ser 120	His	Leu	Ser	Val	Val 125	Ser	Leu	Tyr		
Tyr	Gly 130	Ser	Ile	Phe	Gly	Gln 135	Tyr	Leu	Phe	Pro	Thr 140	Val	Ser	Ser	Ser		
Ile 145	Asp	Lys	Asp	Val	Ile 150	Val	Ala	Leu	Met	Tyr 155	Thr	Val	Asp	Thr	Pro 160		

Met Leu

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ctc tgt ctc gcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat
Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
                                                                          97
            20
gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac
                                                                         145
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
        35
aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg
                                                                         193
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
                         55
gcc ttc tct gac act cga gtt aat gaa tgg gtg ata ttt atc atg gga
                                                                         241
Ala Phe Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
ggg ctc att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca
                                                                         289
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
                 85
aga att gtc tcc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc
                                                                         337
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
            100
aag gcc ctc tct act tgt ggc tcc cac ctg tct gtg gtg tca ctg ttc
                                                                          385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
                                                   125
                              120
                                                                          433
tat gga acc gtt att ggt ctc tac tta tgc tca tca gct aat agt tct
Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser
act cta aag gac act gtc atg gct atg atg tac act gtg gtg acc ccc
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Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
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Met Leu
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Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
                            40
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
Ala Phe Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
                                         75
                    70
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
        115
Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser
                         135
Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
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Met Leu
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                                                                       120
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cttctctatc tccttctcta agtccaacca tqtaqacttc tttttctqtq acctcccacc
                                                                      180
cctgctgaag cttgcctgta gtgaaaccag gccacgggaa tgggtgatct acctctcagc
                                                                      240
ttttctggtc atcacaacca gcatttcagt gattcttaca tcgtacttgt tcatcattca
                                                                      300
gtctattctg aagattcgta cagcaggtgg aaagccaaga ccttctccac ctgtgcttct
                                                                      360
cacaagactg cattgactct cttctttgga acactcatat tcatatacct gaaaggcaac
                                                                      420
atgggcgaat cccttgagga agacaagatc gtgtcaatat tttacactgt ggtcatcccc
                                                                      480
atgcta
                                                                      486
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ggtgaaactg tctttctgtg ggccaaatgt catcagtcac ttcttctgtg atcttccccc
                                                                      180
actgttgaag ctgtcatgtt ctgagacatc tatgaatgaa ttgttgcttt tgatcttctc
                                                                      240
                                                                      300
tqqcattatt qccacqctca cttttttgac tgtggtgatc tcctacatct tcattgttgc
                                                                      360
tgctatcctg aggatccgct aagaagcagg tagacgtaaa gccttctcca cctgcacctc
                                                                      420
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ctcccagtat tccctagaac aagaaaaggt ggtgtctgta ttttataccc tggtggttcc
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tatgtta
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                                                                      120
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cacataattg tggtatcgct ttctttgggt caggtgcttt catgtacctc aaaccacctt
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                                                                           97
gtg tgt acc tta tta gtt ctc tgc tgt tgg gtg gct ggc ttg atg atc
Val Cys Thr Leu Leu Val Leu Cys Cys Trp Val Ala Gly Leu Met Ile
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aat gcc att gat cat ttt agc tgt gat gca ggt cct ctc cta aag atc 193 Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile 50 55 60
tca tgc tca gat aca tgg gta ata gaa cag atg gtt ata ctt atg gct 241 Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Met Val Ile Leu Met Ala 65 70 75 80
gta ttt gca ctc att atc acc cca gtt tgt gtg att ctg tcc tac ttg Val Phe Ala Leu Ile Ile Thr Pro Val Cys Val Ile Leu Ser Tyr Leu 85 90 95
tac ata gtc aga aca att ctg aag ttc cct tct gtt cag caa agg aaa 337 Tyr Ile Val Arg Thr Ile Leu Lys Phe Pro Ser Val Gln Gln Arg Lys 100 105 110
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Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile 50 55 60

Ser 65	Cys	Ser	Asp	Thr	Trp 70	Val	Ile	Glu	Gln	Met 75	Val	Ile	Leu	Met	Ala 80	
Val	Phe	Ala	Leu	Ile 85	Ile	Thr	Pro	Val	Cys 90	Val	Ile	Leu	Ser	Tyr 95	Leu	
туг	Ile	Val	Arg 100	Thr	Ile	Leu	Lys	Phe 105	Pro	Ser	Val	Gln	Gln 110	Arg	Lys	
Lys	Ala	Phe 115	Ser	Thr	Cys	Ser	Ser 120	His	Met	Ile	Val	Val 125	Ser	Ile	Ala	
Tyr	Gly 130	Ser	Cys	Ile	Phe	Ile 135	Tyr	Ile	Lys	Pro	Ser 140	Ala	Lys	Asp	Glu	
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Leu	Leu															
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ctc Leu	tgt Cys	gtc Val	ttc Phe 20	tta Leu	gtg Val	gct Ala	gta Val	act Thr 25	tgg Trp	att Ile	ctg Leu	tct Ser	tgt Cys 30	gcc Ala	agc Ser	97
tcc Ser	ctc Leu	tct Ser 35	cac His	acc Thr	ctt Leu	ctc Leu	ctg Leu 40	acc Thr	cgg Arg	ctg Leu	tct Ser	ttc Phe 45	tgt Cys	gct Ala	gcg Ala	145
aac Asr	acc Thr	ato	ccc Pro	cat His	gtc Val	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	gct Ala	gcc Ala 60	ctg Leu	cto Leu	aag Lys	ctg Leu	193
tco Ser 65	tgc Cys	tca Ser	gat Asp	ato Ile	ttc Phe	ctc Leu	aat Asr	gag Glu	r ctg Lev	ggto Val 75	atg Met	tto Phe	aca Thr	gta Val	ggg Gly 80	241
gto Val	g gtg L Val	g gto Val	att	acc Thr	ctg Leu	cca Pro	tto Phe	ato Met	tgt Cys	ato Ile	cto Lev	g gta ı Val	tca Ser	tat Tyr	ggc Gly	289

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		gly aaa														337
		ttg Leu 115														385
		tca Ser														433
		aag Lys														481
atg Met	-															487
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Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr 115 120 125

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catccagctg cetttetgtg ggcccaatga actggacaac ttetactgtg atgtcctaca
                                                                      180
aatcatcaag ctggcctgca tggacaccta tgtggtagag gtgctggtga tagccaacag
                                                                      240
tggtctgctg tctcttgtct gcttcttggt cttactattc tcttatqcta tcatcctqat
                                                                      300
caccetgaga acaegettet gecagggeca gaacaaggte etetetacet gtgettetea
cctgacagtg gtcagcctga tcttcgtgcc atgcgtattc atctatttga ggcctttctg
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                                                                     120
tgcttcgtct gtccttctgt ggacccaatg acatcaacca cttttactgt gcggacccac
                                                                     180
ccctcttagt cctcgcctgc tcagatactt atgtcaaaga gaccgccatg ttggtggtgg
                                                                     240
ctggttccaa cctcatttgc tctctcaccg tcatcctcat ttcctacact ttcatcttca
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ctgccattct gcgtatccac actgctgagg ggaggcgcaa ggccttctcc acctgcgggt
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360

ctca	tgtga	ac c	gctg	tcac	t gt	cttc	tatg	gga	cact	gtt	ctgc	atgt	ac c	tgag	gcccc	420
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cgat	gtta															488
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ctc Leu	tgc ( Cys (	act Thr	cta Leu 20	ctt Leu	gtg Val	ctg Leu	tgt Cys	gcc Ala 25	tgg Trp	cta Leu	agt Ser	ggg Gly	ttt Phe 30	ctg Leu	acc Thr	97
att Ile	ttc Phe	cca Pro 35	ccc Pro	ctt Leu	atg Met	ctt Leu	ctc Leu 40	ctc Leu	cag Gln	ctg Leu	gat Asp	tac Tyr 45	tgt Cys	gct Ala	tcc Ser	145
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tct Ser 65	tgt Cys	tca Ser	gat Asp	aca Thr	tgg Trp 70	ctc Leu	cta Leu	gaa Glu	gta Val	att Ile 75	ggt Gly	ttt Phe	tac Tyr	ttt Phe	gct Ala 80	241
ttg Leu	gtt Val	act Thr	ttg Leu	ctg Leu 85	ttc Phe	act Thr	ttg Leu	gca Ala	tta Leu 90	gtg Val	att Ile	tta Leu	tct Ser	tac Tyr 95	atg Met	289
tac Tyr	att Ile	atc Ile	agg Arg 100	acc Thr	att Ile	ttg Leu	aga Arg	atc Ile 105	ccg Pro	tct Ser	gcc Ala	agt Ser	caa Gln 110	aga Arg	aaa Lys	337
aag Lys	gct Ala	ttc Phe 115	tcc Ser	act Thr	tgt Cys	tct Ser	tct Ser 120	cac His	atg Met	att Ile	gtc Val	att Ile 125	tcc Ser	att Ile	tct Ser	385
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gca Ala 145	tca Ser	ttg Leu	aca Thr	aaa Lys	gga Gly 150	ata Ile	gct Ala	att Ile	ctc Leu	aat Asn 155	aca Thr	tct Ser	gtt Val	gcc Ala	ccc Pro 160	481
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Asn Val Ile Asp His Phe Ala Cys Asp Tyr Phe Pro Leu Leu Gln Leu
Ser Cys Ser Asp Thr Trp Leu Leu Glu Val Ile Gly Phe Tyr Phe Ala
                    70
Leu Val Thr Leu Leu Phe Thr Leu Ala Leu Val Ile Leu Ser Tyr Met
Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Lys
                                105
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
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Tyr Gly Ser Cys Ile Phe Met Tyr Ala Asn Pro Ser Ala Lys Glu Lys
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Ala Ser Leu Thr Lys Gly Ile Ala Ile Leu Asn Thr Ser Val Ala Pro
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ctc tgt gca ctc atg ctg gcc atg tgc tgg ctg cta acc aac tgt cct
Leu Cys Ala Leu Met Leu Ala Met Cys Trp Leu Leu Thr Asn Cys Pro
gca ttg atg cac acg ctg ttg ctg acc cgt gtg gct ttc tgt gcc cag
                                                                            145
Ala Leu Met His Thr Leu Leu Leu Thr Arg Val Ala Phe Cys Ala Gln
        35
agg gcc atc ccc cac ttc tac tgt gat ccc agt gct ctc ctg aag ctc
                                                                            193
Arg Ala Ile Pro His Phe Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu
gcc tgc tcg gat acc cgc ata aac gag ctg atg atc atc gcc atg ggc
                                                                            241
Ala Cys Ser Asp Thr Arg Ile Asn Glu Leu Met Ile Ile Ala Met Gly
                                            75
                      70
ttg gcc ttc ctc acg gtt ccc ctc acg ctg atc gtc ttc tcc tac gtc
Leu Ala Phe Leu Thr Val Pro Leu Thr Leu Ile Val Phe Ser Tyr Val
                                                                            289
                                       90
                                                                            337
cgc atc tcc tgg gct gtg ctt ggc atc tcg tct cct gga ggg cga tgc
Arg Ile Ser Trp Ala Val Leu Gly Ile Ser Ser Pro Gly Gly Arg Cys
                                                         110
             100
aaa gcc ttc tcc acc tgt ggt tct cat ctc acg gtg gtt ctg ctc ttc
                                                                            385
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Leu Leu Phe
                               120
         115
tat ggg tct ctt atg ggt gtg tat ttg ctt cct ccg tca tct tac tct
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Tyr Gly Ser Leu Met Gly Val Tyr Leu Leu Pro Pro Ser Ser Tyr Ser
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atg t
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Ala Leu Met His Thr Leu Leu Leu Thr Arg Val Ala Phe Cys Ala Gin 40 45

Arg Ala Ile Pro His Phe Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu

Ala Cys Ser Asp Thr Arg Ile Asn Glu Leu Met Ile Ile Ala Met Gly 70

Leu Ala Phe Leu Thr Val Pro Leu Thr Leu Ile Val Phe Ser Tyr Val

Arg Ile Ser Trp Ala Val Leu Gly Ile Ser Ser Pro Gly Gly Arg Cys 105

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Leu Leu Phe 125

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tgtcatcgtg gttaccatgt gctatggaaa gctgtttttt tatgtatgtc aagccctccc	420
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gct ttc tct ctc acc ctt ctg atg act cag ttc tca ttc tgt gcc tcc Ala Phe Ser Leu Thr Leu Leu Met Thr Gln Phe Ser Phe Cys Ala Ser 35 40 45	145
cat too ato caa cac ttt tto tgt gat gta coo coa cto cto aaa ctt His Ser Ile Gln His Phe Phe Cys Asp Val Pro Pro Leu Leu Lys Leu 50 55 60	193
gcc tgt tca gac acc cat atc ttt cag gtc aca atg tta act gaa gga Ala Cys Ser Asp Thr His Ile Phe Gln Val Thr Met Leu Thr Glu Gly 65 70 75 80	241
gtc ctc tca ggt gtg atc cct ctt acc tgt gtc ctg gtc tct tat gcc Val Leu Ser Gly Val Ile Pro Leu Thr Cys Val Leu Val Ser Tyr Ala 85 90 95	289
cac atc atg cac acc atc ctc agg atc cct tct gct ggg ggc aag cac His Ile Met His Thr Ile Leu Arg Ile Pro Ser Ala Gly Gly Lys His 100 105 110	337
aaa gtc ttc tct acc tgt ggc tct cac ctg tca gtg gtc act ctc ttc Lys Val Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Leu Phe 115 120 125	385
tat ggg acc ctc ttt ctg gtg tat ttc cag cct tca tcc tcc tac tca Tyr Gly Thr Leu Phe Leu Val Tyr Phe Gln Pro Ser Ser Ser Tyr Ser 130 135 140	433
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His Ser Ile Gln His Phe Phe Cys Asp Val Pro Pro Leu Leu Lys Leu
Ala Cys Ser Asp Thr His Ile Phe Gln Val Thr Met Leu Thr Glu Gly
Val Leu Ser Gly Val Ile Pro Leu Thr Cys Val Leu Val Ser Tyr Ala
His Ile Met His Thr Ile Leu Arg Ile Pro Ser Ala Gly Gly Lys His
            100
Lys Val Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Leu Phe
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        115
Tyr Gly Thr Leu Phe Leu Val Tyr Phe Gln Pro Ser Ser Ser Tyr Ser
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Met Val
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<220> <221> CDS <222> (2)(487) <223> Product = olfactory receptor
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gtc tgc aga aga ctt gtc ttt tgt tgt tgg gta gct ggt ctg ttt att  Val Cys Arg Arg Leu Val Phe Cys Cys Trp Val Ala Gly Leu Phe Ile  20 25 30
ata atc cct cca ctt agc ctg ggc cta aat ctg gaa ttt tgt gat tct 145 Ile Ile Pro Pro Leu Ser Leu Gly Leu Asn Leu Glu Phe Cys Asp Ser 35 40 45
gat acc att gat cat ttt atc tgt gat gca tct ccc ctc ctg aat atc 193 Asp Thr Ile Asp His Phe Ile Cys Asp Ala Ser Pro Leu Leu Asn Ile 50 55 60
tct tgt tca aat act tgg ttc atg gaa cag act gtt atc atc tgt gca 241 Ser Cys Ser Asn Thr Trp Phe Met Glu Gln Thr Val Ile Ile Cys Ala 65 70 75 80
gtg ctg acc ctc att atg aca ctt atg tgt gta gtt ctg tcc tac att 289 Val Leu Thr Leu Ile Met Thr Leu Met Cys Val Val Leu Ser Tyr Ile 85 90 95
tat atc atc aag aca att tta gga ttc tct tct gcc cag caa aag aaa 337 Tyr Ile Ile Lys Thr Ile Leu Gly Phe Ser Ser Ala Gln Gln Lys Lys 100 105 110
aaa gcc ttt tcc acc tgt tct tcc cac atg att gtg gtg tcc atc acc  Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Thr  115  120  125
tat ggc agc tac atc ttc atc tat atc aaa cct tct gca aag gaa gaa 433 Tyr Gly Ser Tyr Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Glu Glu 130 135 140
gta gcc att aac aag ggt gtg aca gtc ctc act act tcc atc gcc ccc 481 Val Ala Ile Asn Lys Gly Val Thr Val Leu Thr Thr Ser Ile Ala Pro 145 150 155 160
atg ctg Met Leu
<210> 248 <211> 162 <212> PRT <213> Eulemur fulvus
<pre>&lt;220&gt; &lt;221&gt; misc_feature &lt;222&gt; (1)(487) &lt;223&gt; Taxon = 13515; gene = EFU148; Accession DDBJ/EMBL/GenBank = AF179774</pre>
<400> 248

Ile Ile Pro Pro Leu Ser Leu Gly Leu Asn Leu Glu Phe Cys Asp Ser 35 40 45

Asp Thr Ile Asp His Phe Ile Cys Asp Ala Ser Pro Leu Leu Asn Ile 50 55 60

Ser Cys Ser Asn Thr Trp Phe Met Glu Gln Thr Val Ile Ile Cys Ala 65 70 75 80

Val Leu Thr Leu Ile Met Thr Leu Met Cys Val Val Leu Ser Tyr Ile 85 90 95

Tyr Ile Ile Lys Thr Ile Leu Gly Phe Ser Ser Ala Gln Gln Lys Lys 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Thr 115 120 125

Tyr Gly Ser Tyr Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Glu Glu 130 135 140

Val Ala Ile Asn Lys Gly Val Thr Val Leu Thr Thr Ser Ile Ala Pro 145 150 155 160

Met Leu

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<210> 249
<211> 487
<212> DNA
<213> Eulemur fulvus
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<221> misc feature
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<223> Taxon = 13515; gene = EFU149; Accession DDBJ/EMBL/GenBank = AF179775
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<221> CDS
<222>
       (2)..(487)
<223> Product = olfactory receptor
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                                                                       49
  Val Ala Ile Cys Lys Pro Leu His Tyr Arg Val Ile Met Asn Arg Arg
                                      10
gtc tgc aca ctg ctc gtc ttt gcc tct tgg ctg gtt tca ttc tta atc
                                                                       97
```

Val Cys Thr Leu Leu Val Phe Ala Ser Trp Leu Val Ser Phe Leu Ile

gta ttc cca gca ctc atg ttg ctc tta aag ctt gat tac tgt gga ttt 145 Val Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Gly Phe aat att att gac cat ttt acc tgt gat tat ttt ccc ctg ctg cag ctt 193 Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu 55 tcc tgt tca gat aca aaa ttc ctg gag ata atg ggg ttt tcc tgt gct 241 Ser Cys Ser Asp Thr Lys Phe Leu Glu Ile Met Gly Phe Ser Cys Ala gtg ttt act cta atg ttc act ttg gca tta ata ttt ctg tcc tac atg 289 Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Phe Leu Ser Tyr Met cac atc gtg aga acg att ttg aga att cct tct act agt cag agg aca 337 His Ile Val Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr 105 100 aag gcc ttt tct aca tgt tct tcc cac atg att gtc atc tcc atc tct 385 Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser 120 tat ggc agc tgc att ttt atg tac att aag ccc tca gca aag gat aga 433 Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg 135 140 gta tot ttg ago aag goa gtg got gtg cta atc acc tca gta got ccc 481 Val Ser Leu Ser Lys Ala Val Ala Val Leu Ile Thr Ser Val Ala Pro 155 150 487 . atg ctc Met Leu <210> 250 <211> 162 <212> PRT <213> Eulemur fulvus <220> <221> misc\_feature (1) . . (487)<222> Taxon = 13515; gene = EFU149; Accession DDBJ/EMBL/GenBank = AF179775 <223> <400> 250 Val Ala Ile Cys Lys Pro Leu His Tyr Arg Val Ile Met Asn Arg Arg : 5 Val Cys Thr Leu Leu Val Phe Ala Ser Trp Leu Val Ser Phe Leu Ile 20

and the second of the second o

Val Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Gly Phe

Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu 50 55 60





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Ser Cys Ser Asp Thr Lys Phe Leu Glu Ile Met Gly Phe Ser Cys Ala

Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Phe Leu Ser Tyr Met 90

His Ile Val Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr 105

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser 120

Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg 130

Val Ser Leu Ser Lys Ala Val Ala Val Leu Ile Thr Ser Val Ala Pro 160

Met Leu

<210> 251

<211> 484

<212> DNA

<213> Eulemur fulvus

<220>

<221> misc\_feature

<222> (1)..(484)

<223> Taxon = 13515; gene = EFU150; pseudogene; Accession DDBJ/EMBL/GenBank = AF179776

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<210> 252

<211> 487

<212> DNA

<213> Eulemur fulvus

<220>

<400> 253

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<223> Taxon = 13515; gene = EFU151; Accession DDBJ/EMBL/GenBank = AF179777
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      CDS
      (2)..(487)
<222>
      Product = olfactory receptor
<223>
<400> 252
t ctg gct atc tgc tat cct cta cac tac agg aca atc atg agc agc ctg
                                                                       49
 Leu Ala Ile Cys Tyr Pro Leu His Tyr Arg Thr Ile Met Ser Ser Leu
                                                                       97
ctg gct aca cag ctg gcc ttg ggc tcc tgg gtc tgt ggt ttc ctg gcc
Leu Ala Thr Gln Leu Ala Leu Gly Ser Trp Val Cys Gly Phe Leu Ala
            20
att gca gtg ctg acg gcc ctt atc agt ggc ctg tcc ttc tgt ggc gcc
                                                                      145
Ile Ala Val Leu Thr Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Ala
                            40
                                                                      193
cgt gcc atc aac cac ttc ttc tgt gac att gca ccc tgg att gcc ctg
Arg Ala Ile Asn His Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu
gcc tgc acc agc aca cag gca ata gag ctc gtg gcc ttt gtg att gct
                                                                      241
Ala Cys Thr Ser Thr Gln Ala Ile Glu Leu Val Ala Phe Val Ile Ala
                                         75
                    70
ttt gtg gtc atc ctg agt tca tgc ctc atc acc ctg gtc tcc tac gtg
                                                                      289
Phe Val Val Ile Leu Ser Ser Cys Leu Ile Thr Leu Val Ser Tyr Val
                                                         95
                85
tac att atc agc acc atc ctc agg atc cca tct gcc agc ggc cgg agc
                                                                      337
Tyr Ile Ile Ser Thr Ile Leu Arg Ile Pro Ser Ala Ser Gly Arg Ser
                                 105
aaa gcc ttc tct acg tgc tcc tct cac ctc acc gtg gtg ctc atc tgg
                                                                      385
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp
                             120
        115
tat ggg tcc acg att ttt ctt cat gtc cgc acc tcc atc aca gac gcc
                                                                       433
Tyr Gly Ser Thr Ile Phe Leu His Val Arg Thr Ser Ile Thr Asp Ala
    130
                                                                       481
ttg gat ctg acc aaa gct gtc cat gtc ctg aac acc gtg gtg act cca
Leu Asp Leu Thr Lys Ala Val His Val Leu Asn Thr Val Val Thr Pro
                                         155
                     150
                                                                       487
gtt cta
Val Leu
<210> 253
<211>
       162
<212>
       PRT
<213> Eulemur fulvus
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       misc_feature
<221>
       (1)..(487)
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      Taxon = 13515; gene = EFU151; Accession DDBJ/EMBL/GenBank = AF179777
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Leu Ala Ile Cys Tyr Pro Leu His Tyr Arg Thr Ile Met Ser Ser Leu 1 5 10 15
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Leu Ala Thr Gln Leu Ala Leu Gly Ser Trp Val Cys Gly Phe Leu Ala 20 25 30

Ile Ala Val Leu Thr Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Ala 35 40 45

Arg Ala Ile Asn His Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu 50 55 60

Ala Cys Thr Ser Thr Gln Ala Ile Glu Leu Val Ala Phe Val Ile Ala 65 70 75 80

Phe Val Val Ile Leu Ser Ser Cys Leu Ile Thr Leu Val Ser Tyr Val 85 90 95

Tyr Ile Ile Ser Thr Ile Leu Arg Ile Pro Ser Ala Ser Gly Arg Ser 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp 115 120 125

Tyr Gly Ser Thr Ile Phe Leu His Val Arg Thr Ser Ile Thr Asp Ala 130 135 140

Leu Asp Leu Thr Lys Ala Val His Val Leu Asn Thr Val Val Thr Pro 145 150 155 160

Val Leu

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<210> 254
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<220>

<221> misc\_feature

<222> (1)..(487)

<223> Taxon = 13515; gene = EFU153; Accession DDBJ/EMBL/GenBank = AF179778

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 254

t gtt gct atc tgt aag ccc ctg cat tac agg gtc atc atg aat cga aga
Val Ala Ile Cys Lys Pro Leu His Tyr Arg Val Ile Met Asn Arg Arg

1 5 10 15

gtc tgc aca ctg ctc gtc ttt gcc tct tgg ctg gtt tca ttc tta atc

<sup>&</sup>lt;211> 487

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Eulemur fulvus

Val Cys Th	nr Leu Le 20	u Val Phe	Ala Se		Leu	Val	Ser	Phe 30	Leu	Ile	
gta ttc co Val Phe Pi 35	o Ala Le	c atg ttg u Met Lev	ctc tt Leu Le 40	a aag eu Lys	ctt Leu	gat Asp	tac Tyr 45	tgt Cys	gga Gly	ttt Phe	145
aat att at Asn Ile II 50	t gac ca le Asp Hi	t ttt acc s Phe Thr 55	tgt ga Cys As	it tat sp Tyr	ttt Phe	ccc Pro 60	ctg Leu	ctg Leu	cag Gln	ctt Leu	193
tcc tgt to Ser Cys Se 65	ca gat ac er Asp Th	a aaa tto r Lys Phe 70	ctg ga Leu Gl	ag ata Lu Ile	atg Met 75	gly ggg	ttt Phe	tcc Ser	tgt Cys	gct Ala 80	241
gtg ttt ac Val Phe Th	ct cta at nr Leu Me 85	t Phe Thr	ttg go Leu Al	ca tta la Leu 90	ata Ile	ttt Phe	ctg Leu	tcc Ser	tac Tyr 95	atg Met	289
cac atc go	tg agg ac al Arg Th 100	g att tto r Ile Lev	ı Arg Il	t cct le Pro 05	tct Ser	act Thr	agt Ser	cag Gln 110	agg Arg	aca Thr	337
aag gcc t Lys Ala P	tt tct ac he Ser Th 15	a tgt tct r Cys Sei	tcc ca Ser Hi 120	ac atg is Met	att Ile	gtc Val	atc Ile 125	tcc Ser	atc Ile	tct Ser	385
tat ggc a Tyr Gly S 130	gc tgc at er Cys Il	t ttt atg e Phe Mei 13!	Tyr I	tt aag le Lys	ccc Pro	tca Ser 140	gca Ala	aaa Lys	gat Asp	aga Arg	433
gta tct t Val Ser L 145	tg agc aa eu Ser Ly	g gca gtg s Ala Va 150	g gct g L Ala Va	tg cta al Leu	atc Ile 155	acc Thr	tca Ser	gta Val	gct Ala	ccc Pro 160	481
atg ctc Met Leu											487
<210> 25 <211> 16 <212> PR <213> Eu	2	.vus									
-222 (1	sc_featur )(487) .xon = 135		= EFU1	53; Ac	cess	ion	DDBJ	/EMB	L/Ge	nBank = 1	AF179778
<400> 25	5										
Val Ala I 1	le Cys Ly 5	ys Pro Le	u His T	yr Arg 10	y Val	Ile	Met	Asn	Arg 15	Arg	
Val Cys T	chr Leu Le 20	eu Val Ph		er Trp 5	Leu	Val	Ser	Phe 30	Leu	Ile	
Val Phe E	Pro Ala Lo 35	eu Met Le	u Leu L 40	eu Lys	s Leu	. Asp	Tyr 45	Сув	Gly	Phe	
Asn Ile 1	[le Asp H	is Phe Th 55		sp Tyr	Phe	Pro 60	Leu	Leu	Gln	Leu	

Ser Cys Ser Asp Thr Lys Phe Leu Glu Ile Met Gly Phe Ser Cys Ala 70 75 80
Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Phe Leu Ser Tyr Met 85 90 95
His Ile Val Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr 100 105 110
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser 115 120 125
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg 130 135 140
Val Ser Leu Ser Lys Ala Val Ala Val Leu Ile Thr Ser Val Ala Pro 145 150 155 160
Met Leu
<210> 256 <211> 488 <212> DNA <213> Eulemur fulvus
<pre>&lt;220&gt; &lt;221&gt; misc_feature &lt;222&gt; (1)(488) &lt;223&gt; Taxon = 13515; gene = EFU154; Accession DDBJ/EMBL/GenBank = AF179779</pre>
<220> <221> CDS <222> (2)(487) <223> Product = olfactory receptor
<pre>&lt;400&gt; 256 c atg gcc atc tgc cat ccg ctc cgt tac cct gtc ttc atg aac cac agg</pre>
gtg tgt ctc ttc ctg gca tct ggc tgc tgg ttc ctg gga tca gta gat Val Cys Leu Phe Leu Ala Ser Gly Cys Trp Phe Leu Gly Ser Val Asp 20 25 30
ggc ttc atg ctc act cca atc acc atg acc ttc ccc tac tgc agg tcc  Gly Phe Met Leu Thr Pro Ile Thr Met Thr Phe Pro Tyr Cys Arg Ser  35 40 45
cgg gag att cac cat tcc ttc tgc gaa gtc cct gct gta acg acg ctt 193 Arg Glu Ile His His Ser Phe Cys Glu Val Pro Ala Val Thr Thr Leu 50 55 60
tcc tgc tca gac acc tca ctc tat gaa atg ctc atg tac ctg tgc tgt  Ser Cys Ser Asp Thr Ser Leu Tyr Glu Met Leu Met Tyr Leu Cys Cys  70  75  80

gtc ctc atg ctc ctc att cct gtg aca gtc att tca agc tcc tat tca Val Leu Met Leu Leu Ile Pro Val Thr Val Ile Ser Ser Ser Tyr Ser 85 90 95	289
ttc att ctc ctc acc atc cac agg atg ggc tca gca gag ggc cgg aag Phe Ile Leu Leu Thr Ile His Arg Met Gly Ser Ala Glu Gly Arg Lys 100 105 110	337
aag gcc ttt gcc acc tgt tcc tcc cac atg acc gtg gtt atc ctc ttc Lys Ala Phe Ala Thr Cys Ser Ser His Met Thr Val Val Ile Leu Phe 115 120 125	385
tat ggg gcc gcc atc tac acc tac atg ctc ccc agc tcc tac cac act Tyr Gly Ala Ala Ile Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr 130 135 140	433
cct gag aag gac atg atg gtg tct gtc ttt tat acc atc cta act cct Pro Glu Lys Asp Met Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro 145 150 155 160	481
gtg cta a Val Leu	488
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<pre>&lt;223&gt; Taxon = 13515; gene = EFU154; Accession DDBJ/EMBL/GenBank =</pre>	= AF179779
<pre>&lt;223&gt; Taxon = 13515; gene = EFU154; Accession DDBJ/EMBL/GenBank = &lt;400&gt; 257  Met Ala Ile Cys His Pro Leu Arg Tyr Pro Val Phe Met Asn His Arg 1 5 10 15</pre>	= AF179779
<pre>&lt;223&gt; Taxon = 13515; gene = EFU154; Accession DDBJ/EMBL/GenBank = &lt;400&gt; 257  Met Ala Ile Cys His Pro Leu Arg Tyr Pro Val Phe Met Asn His Arg 1</pre>	= AF179779
<pre> &lt;223&gt; Taxon = 13515; gene = EFU154; Accession DDBJ/EMBL/GenBank = &lt;400&gt; 257  Met Ala Ile Cys His Pro Leu Arg Tyr Pro Val Phe Met Asn His Arg 1</pre>	= AF179779
<pre>&lt;223&gt; Taxon = 13515; gene = EFU154; Accession DDBJ/EMBL/GenBank = &lt;400&gt; 257  Met Ala Ile Cys His Pro Leu Arg Tyr Pro Val Phe Met Asn His Arg 1</pre>	= AF179779
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115 120 125

Tyr Gly Ala Ala Ile Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr 130 140

Pro Glu Lys Asp Met Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro 145 150 155 160

Val Leu

<210> 258 <211> 488 <212> DNA <213> Eulemur fulvus <220>

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<223> Taxon = 13515; gene = EFU155; pseudogene; Accession DDBJ/EMBL/GenBank = AF179780

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<210> 259 <211> 486

<212> DNA

<213> Eulemur fulvus

<220>

<221> misc\_feature

<222> (1)..(486)

<223> Taxon = 13515; gene = EFU156; pseudogene; Accession DDBJ/EMBL/GenBank = AF179781

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tctcatcatc tgttgttggg tggctggttt atgcataata atccctccac ttagcctggg 120
tttaaatcta aaattctgtg actctaacat gattgatcat tttggttgcg atgcatttcc 180
cctggtgaaa atctcatgct cagacacatg gttcatggaa cagacggtta tcatctgtgc 240

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tgtgctgacc ctgaatatga ctctaacttg tgtagttctg tcatacgctt acatcatcaa
                                                                     300
gacaattttt agatteeett etgteeagea aaggaaaaag geetttteea eetgttette
                                                                     360
ccacatgatt gtggtttcca tcacctatgg cacgtgcatt ttcatctaca tgaatcctac
                                                                     420
agcaaaggaa gaagtgaccg ttaataaagt agtttctttg ctcatttctt ctattttgct
                                                                     480
acattq
                                                                     486
<210>
      260
<211>
      486
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<213> Eulemur rubriventer
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= AF179782
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                                                                      60
catgctggcc atgtgctggc tgctaaccag ctgtcctgcg ttgatgcaca cgctgttgct
                                                                     120
gaccogtgtg gctttctgtg cocagaaggc catcocccac ttctactgtg atcccagtgc
                                                                     180
teteetgaag etegeetget eggataceeg cataaatgag etgatgatea tegeeatggg
                                                                     240
cttgacgttc ctcactattc ccctcacact gatcgtcttc tcctacgtcc gcatctcctg
                                                                     300
ggctgtgctt ggcatctcgt ctcctggcgg gcgatgcaag gccttctcca cctgtggttc
                                                                     360
tcatctcacg gtggttctgc tcttctatgg gtctcttatg ggtgtgtatt tgcttcctcc
                                                                     420
gtcatcttac tctacagaga gggaaagcag gctgccattc tctacatggt gatcattccc
                                                                     480
atgtta
                                                                     486
<210> 261
<211> 484
<212> DNA
<213> Eulemur rubriventer
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<221> misc feature
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<222> Taxon = 34829; gene = ERU159; pseudogene; Accession DDBJ/EMBL/GenBank
= AF179783
<400> 261
tqtqqccatc tqcaacccac tqaqqtatcc catcatcatq aacagggtgt tataagtgca
                                                                      60
                                                                     120
aatggetgea tggtettgga teataggeta tetgatetee ttagtgeaaa eagtettgae
aatgatattg cctttctgtg gcaataatgt cattgatcat attacctgtg agatcctggc
                                                                     180
                                                                     240
tettaaaete atatgeteag atattteeat gaatgtgett ateatggeag tggeaagtat
                                                                     300
tgttatattg gtgattcctc tgctgttcat ttttatctcc tatgtattca tcctctcttc
catcctgaga attaattctt ctgaggggag aaagaaagcc tttgcaacct gttcagccca
                                                                     360
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cotgactgtg gtoatottat totatggtto agototttt atgtacatga agootaagto	420
aaagtacaca aaagtatetg atgaaateat tgeaetgtet taeggagtag taaceceaat	480
gttg	484
<210> 262 <211> 487 <212> DNA <213> Eulemur rubriventer	
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ctc tgc acc tta ttg gtg gct ata tcc tgg ctc ctg tct tgt gcc agc Leu Cys Thr Leu Leu Val Ala Ile Ser Trp Leu Leu Ser Cys Ala Ser 20 25 30	97
tcc ctc tcc cac acc ctt ctc ctg acc cgg ctg tcc ttc tgt gct gct Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala 35 40 45	145
aat gtc att ccc aac ttc ttc tgt gac ctt gct gct ctg ctc aag ctg Asn Val Ile Pro Asn Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60	193
tcc tgc tca gac atc ttc ctc aat gag ctg gtc atg ttt aca gta ggg Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80	241
gtg gtg gtc att acc ttg cca ttc tta tgt atc ctg gta tct tac ggc Val Val Val Ile Thr Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 85 90 95	289
tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc tgc Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Cys 100 105 110	337
aaa gca tta tcc acg tgt ggg tcc cat ctc tct gtg gtg tct ctg tac Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr 115 120 125	385
tac ggg gca ata ttt ggg cag tac ctt ttc cca gca tta agc aat tcc Tyr Gly Ala Ile Phe Gly Gln Tyr Leu Phe Pro Ala Leu Ser Asn Ser 130 135 140	433
att gac aag gac atc att gtg gct atg atg tac acg gtg gtc aca ccc Ile Asp Lys Asp Ile Ile Val Ala Met Met Tyr Thr Val Val Thr Pro 145 150 150	481
atg ttg Met Leu	487

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<210> 263
<211> 162
<212> PRT
<213> Eulemur rubriventer
<220>
<221> misc feature
<222> (1)..(487)
<223> Taxon = 34829; gene = ERU160; Accession DDBJ/EMBL/GenBank = AF179784
<400> 263
Val Ala Ile Cys His Pro Leu His Tyr Thr Thr Ile Met Arg Glu Glu
Leu Cys Thr Leu Leu Val Ala Ile Ser Trp Leu Leu Ser Cys Ala Ser
Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
Asn Val Ile Pro Asn Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
Val Val Ile Thr Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Cys
                               105
            100
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
                                                125
        115
                            120
Tyr Gly Ala Ile Phe Gly Gln Tyr Leu Phe Pro Ala Leu Ser Asn Ser
    130
                        135
Ile Asp Lys Asp Ile Ile Val Ala Met Met Tyr Thr Val Val Thr Pro
                                        155
Met Leu
<210> 264
<211> 475
<212> DNA
<213> Eulemur rubriventer
<220>
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<221> misc\_feature <222> (1)..(475)

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<221> CDS
<222> (2)..(475)
<223> Product = olfactory receptor
c gtg gca atc tgc aag cct ctt cat tac atg aat att atg agt cgt caa
 Val Ala Ile Cys Lys Pro Leu His Tyr Met Asn Ile Met Ser Arg Gln
                                       10
                                                                         97
ctg tgt cac ctt ctg gtg gct ggt tcc tgg ctg gga ggc ttt ctt cac
Leu Cys His Leu Leu Val Ala Gly Ser Trp Leu Gly Gly Phe Leu His
tet att att cag att ttt atc acc atc caa teg cee ttt tgt ggt eec
                                                                         145
Ser Ile Ile Gln Ile Phe Ile Thr Ile Gln Ser Pro Phe Cys Gly Pro
aac gtg att gac cac tac ttc tgt gac ctc ctg cca tta ttc aag ctt
                                                                         193
Asn Val Ile Asp His Tyr Phe Cys Asp Leu Leu Pro Leu Phe Lys Leu
gcc tgc acc gac acc ttt gta gag ggg ctg act gtg ttg gcc aat agt
                                                                         241
Ala Cys Thr Asp Thr Phe Val Glu Gly Leu Thr Val Leu Ala Asn Ser
                                          75
                                                                         289
ggc tta att ccc gtg tgc tcc ctg ttt atc ctg gtg tcc tcc tat atc
Gly Leu Ile Pro Val Cys Ser Leu Phe Ile Leu Val Ser Ser Tyr Ile
                                                                         337
att att ctg gtg cac ttg agg aaa cat tct gca gag ggg agg cac aaa
Ile Ile Leu Val His Leu Arg Lys His Ser Ala Glu Gly Arg His Lys
             100
gcc ctc tct acc tgt gcc tct cac atc acg gtg gtc att ttg ttt ttt Ala Leu Ser Thr Cys Ala Ser His Ile Thr Val Val Ile Leu Phe Phe
                                                                         385
        115
                              120
gga cet gee ate tte etc tac atg ega eet tee tet ace tte aca gaa
                                                                         433
Gly Pro Ala Ile Phe Leu Tyr Met Arg Pro Ser Ser Thr Phe Thr Glu
                         135
gac aaa ctc atg ggt gtg ttg tac aca gtc atc acc ccc agt
                                                                         475
Asp Lys Leu Met Gly Val Leu Tyr Thr Val Ile Thr Pro Ser
                                          155
                     150
<210> 265
<211> 158
<212>
       PRT
<213> Eulemur rubriventer
<220>
<221> misc_feature
 <222>
        (1)...(475)
        Taxon = 34829; gene = ERU161; Accession DDBJ/EMBL/GenBank = AF179785
<223>
<400> 265
 Val Ala Ile Cys Lys Pro Leu His Tyr Met Asn Ile Met Ser Arg Gln
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Leu Cys His Leu Leu Val Ala Gly Ser Trp Leu Gly Gly Phe Leu His

Ser	Ile	Ile	Gln	Ile	Phe	Ile	Thr	Ile	Gln	Ser	Pro	Phe	Cys	Gly	Pro
		35					40					45			

Asn Val Ile Asp His Tyr Phe Cys Asp Leu Leu Pro Leu Phe Lys Leu 50 55 60

Ala Cys Thr Asp Thr Phe Val Glu Gly Leu Thr Val Leu Ala Asn Ser 70 75 80

Gly Leu Ile Pro Val Cys Ser Leu Phe Ile Leu Val Ser Ser Tyr Ile 85 90 95

Ile Ile Leu Val His Leu Arg Lys His Ser Ala Glu Gly Arg His Lys
100 105 110

Ala Leu Ser Thr Cys Ala Ser His Ile Thr Val Val Ile Leu Phe Phe 115 120 125

Gly Pro Ala Ile Phe Leu Tyr Met Arg Pro Ser Ser Thr Phe Thr Glu 130 135 140

Asp Lys Leu Met Gly Val Leu Tyr Thr Val Ile Thr Pro Ser

<210> 266

<211> 487

<212> DNA

<213> Eulemur rubriventer

<220>

<221> misc\_feature

<222> (1)..(487)

<223> Taxon = 34829; gene = ERU162; Accession DDBJ/EMBL/GenBank = AF179786

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 266

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Val Ala Ile Ser Asn Pro Pro Leu Tyr Val Gln Ala Met Pro Arg Lys
10 15

ctg tgc atc tgt ttc att atc tgt tca tac act gga ggc ttt gtt aat 97 Leu Cys Ile Cys Phe Ile Ile Cys Ser Tyr Thr Gly Gly Phe Val Asn 25 30

gca ata ata tta acc agc aac aca ttc acg ttg gat ttt tgt ggt gac 145
Ala Ile Ile Leu Thr Ser Asn Thr Phe Thr Leu Asp Phe Cys Gly Asp
35 40 45

aat gtc atc gac gac ttt ttc tgt gat gtc cca ccc ctg gtg aag ttg
Asn Val Ile Asp Asp Phe Phe Cys Asp Val Pro Pro Leu Val Lys Leu
50 55 60

gcc tgt gat gtg gaa ggg agc tac cag gct gtg ctg tac ttc ctc ctgAla Cys Asp Val Glu Gly Ser Tyr Gln Ala Val Leu Tyr Phe Leu Leu65707580	241
gcc tcc aac gtc atc tcc ccg gcc atg ctc atc ctc gcc tcc tac gtc Ala Ser Asn Val Ile Ser Pro Ala Met Leu Ile Leu Ala Ser Tyr Val 85 90 95	289
ttc atc atc gca gca gtc ttg agg gtc cgc tcc agc cgg ggc cgc ctc Phe Ile Ile Ala Ala Val Leu Arg Val Arg Ser Ser Arg Gly Arg Leu 100 105 110	337
aag gcc ttc tcc acg tgc tcc tcc cac ctg atc tct gtt acc tta tac Lys Ala Phe Ser Thr Cys Ser Ser His Leu Ile Ser Val Thr Leu Tyr 115 120 125	385
tac ggc tcc att ctc tac atc tac tct cgc cca agt tcc agc tat tcc Tyr Gly Ser Ile Leu Tyr Ile Tyr Ser Arg Pro Ser Ser Ser Tyr Ser 130 135 140	433
ctc gag agg gac aaa atg gtc tct acc ttt tac acc gtg ctg ttc ccc Leu Glu Arg Asp Lys Met Val Ser Thr Phe Tyr Thr Val Leu Phe Pro 145 150 155	481
acg ctc Thr Leu	487
<210> 267 <211> 162 <212> PRT	
<213> Eulemur rubriventer <220>	e
<pre>&lt;213&gt; Eulemur rubriventer  &lt;220&gt; &lt;221&gt; misc_feature &lt;222&gt; (1)(487) &lt;223&gt; Taxon = 34829; gene = ERU162; Accession DDBJ/EMBL/GenBank =</pre>	= AF179786
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<pre>&lt;220&gt; &lt;221&gt; misc_feature &lt;222&gt; (1)(487) &lt;223&gt; Taxon = 34829; gene = ERU162; Accession DDBJ/EMBL/GenBank =</pre>	: = AF179786
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Phe Ile Ile Ala Ala Val Leu Arg Val Arg Ser Ser Arg Gly Arg Leu 100 105 110
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Lys Ala Phe Ser Thr Cys Ser Ser His Leu Ile Ser Val Thr Leu Tyr 115 120 125

Tyr Gly Ser Ile Leu Tyr Ile Tyr Ser Arg Pro Ser Ser Ser Tyr Ser 130 135 140

Leu Glu Arg Asp Lys Met Val Ser Thr Phe Tyr Thr Val Leu Phe Pro 145 150 155 160

Thr Leu

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<210> 268
<211> 478
<212> DNA
<213> Eulemur rubriventer
<220>
<221> misc_feature
<222>
      (1)..(478)
<223> Taxon = 34829; gene = ERU163; Accession DDBJ/EMBL/GenBank = AF179787
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      CDS
<221>
<222>
      (2)..(478)
<223> Product = olfactory receptor
<400> 268
t gtt gcc gta tgt aac cct ttg cat tac ctg acg gtc atg aac cgc cag
                                                                          49
  Val Ala Val Cys Asn Pro Leu His Tyr Leu Thr Val Met Asn Arg Gln
                                        10
ctc tgc ctt cag ttg gtt ttt gcc tgc tgg tgt ggg ggt ttc atc cac
                                                                          97
Leu Cys Leu Gln Leu Val Phe Ala Cys Trp Cys Gly Gly Phe Ile His
tot gte aca cag gtt ata etg gte ate cag etg ece tte tgt gge ece
                                                                         145
Ser Val Thr Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro
aac aaa ttg gac agt ttc tac tgt gat gtc cca gag gtc atc aag ctg
                                                                          193
Asn Lys Leu Asp Ser Phe Tyr Cys Asp Val Pro Glu Val Ile Lys Leu
gcc tgc ctg gac acc tat gtg gta gaa gtg ctg atg gtt acc aac agt
                                                                          241
Ala Cys Leu Asp Thr Tyr Val Val Glu Val Leu Met Val Thr Asn Ser
65
                     70
                                                                          289
ggt ctg cta tct ctt gtc tgc ttc ttg gtc ttg ata ttc tct tat gcc
Gly Leu Leu Ser Leu Val Cys Phe Leu Val Leu Ile Phe Ser Tyr Ala
ace ate etg ace ace etg aga act ege etc eac eag gge eag age aag
                                                                          337
Thr Ile Leu Thr Thr Leu Arg Thr Arg Leu His Gln Gly Gln Ser Lys
                                  105
gcc ttc tct acc tgt gcc tcc cac cta atg gtg gtc agc ctg atc ttt
Ala Phe Ser Thr Cys Ala Ser His Leu Met Val Val Ser Leu Ile Phe
                                                                          385
```

lu.

gtg Val	cca Pro 130	tgt Cys	gta Val	ttc Phe	atc Ile	tac Tyr 135	Leu	agg Arg	cct Pro	ttc Phe	tgc Cys 140	agc Ser	ttc Phe	tct Ser	gtg Val	43:
------------	-------------------	------------	------------	------------	------------	-------------------	-----	------------	------------	------------	-------------------	------------	------------	------------	------------	-----

gat aag ata ttc tct gtg ttt tac atg gtg atc aca cct atg ttg
Asp Lys Ile Phe Ser Val Phe Tyr Met Val Ile Thr Pro Met Leu
145
150
155

<210> 269 <211> 159

<212> PRT

<213> Eulemur rubriventer

<220>

<221> misc\_feature

115

<222> (1)..(478)

<223> Taxon = 34829; gene = ERU163; Accession DDBJ/EMBL/GenBank = AF179787

<400> 269

Val Ala Val Cys Asn Pro Leu His Tyr Leu Thr Val Met Asn Arg Gln
1 10 15

Leu Cys Leu Gln Leu Val Phe Ala Cys Trp Cys Gly Gly Phe Ile His 20 25 30

Ser Val Thr Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro 35 40 45

Asn Lys Leu Asp Ser Phe Tyr Cys Asp Val Pro Glu Val Ile Lys Leu 50 55 60

Ala Cys Leu Asp Thr Tyr Val Val Glu Val Leu Met Val Thr Asn Ser 65 70 75 80

Gly Leu Leu Ser Leu Val Cys Phe Leu Val Leu Ile Phe Ser Tyr Ala 85 90 95

Thr Ile Leu Thr Thr Leu Arg Thr Arg Leu His Gln Gly Gln Ser Lys 100 105 110

Ala Phe Ser Thr Cys Ala Ser His Leu Met Val Val Ser Leu Ile Phe 115 120 125

Val Pro Cys Val Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val 130 135 140

Asp Lys Ile Phe Ser Val Phe Tyr Met Val Ile Thr Pro Met Leu 145 150 155

<210> 270

<211> 487

<212> DNA

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<213> Eulemur rubriventer
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 34829; gene = ERU164; Accession DDBJ/EMBL/GenBank = AF179788
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 270
t gtg gcc atc tgc aaa cct ctt cat tac aca acc atc att agc acc agg
                                                                          49
  Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Ile Ser Thr Arg
                                        10
                                                                          97
gtt tgt atc ctt ctt gtc tgt agc tcc tgg ctt gca gga ttc ttg atc
Val Cys Ile Leu Leu Val Cys Ser Ser Trp Leu Ala Gly Phe Leu Ile
                                  25
atc ttt cca cca ata atc ctt ctt ctg cag ttg gac ttc tgt gcc tcc
                                                                         145
Ile Phe Pro Pro Ile Ile Leu Leu Leu Gln Leu Asp Phe Cys Ala Ser
                                                                         193
aat ata att gat cat ttt atc tgt gat tct tct cca att ctg cag ctt
Asn Ile Ile Asp His Phe Ile Cys Asp Ser Ser Pro Ile Leu Gln Leu
                         55
    50
tet tgt aca aac act cac ttt cta gaa ctc atg gca ttt tgt tta gcc
                                                                          241
Ser Cys Thr Asn Thr His Phe Leu Glu Leu Met Ala Phe Cys Leu Ala
gtg gtg aca ctc atg gtc acc ttg acc tta gtt att ctc tcc tat aca Val Val Thr Leu Met Val Thr Leu Thr Leu Val Ile Leu Ser Tyr Thr
                                                                          289
                                      90
aat att atc cgg aca att cta aga att cct tct atg agt caa agg aaa
                                                                          337
Asn Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Met Ser Gln Arg Lys
             100
aaa gcc ttt tcc act tgt tcc tcc cat ata ata gtt gtt tcc ctc tct
                                                                          385
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Ser
                              120
         115
tat ggt agt tgt atc ttc atg tac ata aag cct tct aca agg gaa agg
                                                                          433
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Thr Arg Glu Arg
                          135
                                                                          481
gtg act tta agc aaa gga gta gct gtg gtt aat act tca gtg gct cct
Val Thr Leu Ser Lys Gly Val Ala Val Val Asn Thr Ser Val Ala Pro
                      150
                                           155
145
                                                                          487
ctt ttg
Leu Leu
 <210> 271
 <211> 162
 <212>
       PRT
 <213> Eulemur rubriventer
 <220>
 <221> misc_feature <222> (1)..(487)
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<223> Taxon = 34829; qene = ERU164; Accession DDBJ/EMBL/GenBank = AF179788 <400> 271

Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Ile Ser Thr Arg 15

Val Cys Ile Leu Leu Val Cys Ser Ser Trp Leu Ala Gly Phe Leu Ile

Ile Phe Pro Pro Ile Ile Leu Leu Leu Gln Leu Asp Phe Cys Ala Ser

Asn Ile Ile Asp His Phe Ile Cys Asp Ser Ser Pro Ile Leu Gln Leu

Ser Cys Thr Asn Thr His Phe Leu Glu Leu Met Ala Phe Cys Leu Ala 75

Val Val Thr Leu Met Val Thr Leu Thr Leu Val Ile Leu Ser Tyr Thr 85

Asn Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Met Ser Gln Arg Lys 105

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Ser 120

Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Thr Arg Glu Arg

Val Thr Leu Ser Lys Gly Val Ala Val Val Asn Thr Ser Val Ala Pro 160 150

Leu Leu

<210> 272

<211> 483

<212> DNA

<213> Eulemur rubriventer

<220>

<221> misc\_feature

(1)..(483) <222>

<223> Taxon = 34829; gene = ERU165; pseudogene; Accession DDBJ/EMBL/GenBank = AF179789

<400> 272

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ageteatect egectgetgg etggeagggt teteetteat cattgtgeet gteateetga 120

ccagtcagct tccattctgt gacacccaca tcaaccactt cttctgtgac tatacacctc 180

taat	ggag	gr 99	grere	gcag	999	geca	aayy	tge	cyga	yaı	9919	gatti	. c a		ggccc	240
tggt	ggca	ct g	ctca	gcac	c tt	ggtg	ctga	tca	ccct	gtc	ctac	atcca	ag a	tcat	cagga	300
cgati	tgtc	ag ga	atcc	cctct	gt	ccag	gaga	gga	aaaa	ggc	tttc	tccad	cc t	gttc	ctccc	360
atgt	catc	gt g	gtta	ccat	g tg	ctate	ggaa	gct	gttt	ttt	tatg	tatgt	cc a	agcc	ctccc	420
cagg	caaa	gg g	gttg	atcta	a aa	caaa	ggag	tgt	ctta	atc	aata	caatt	ta t	tgcc	cccct	480
ctt																483
<210 <211 <212 <213	> 4 > D	73 86 NA ulem	ur r	ubri	vent	er										
<220 <221 <222 <223	> m	isc_ 1) axon	(486	)	; ge	ne =	ERU	167;	Acc	essi	on D	DBJ/	EMBL	/Gen	Bank =	= <b>AF179</b> 790
<220 <221 <222 <223	> C	DS 2) rodu		) olf	acto	ry r	ecep	tor								
<400 t gt Va 1	a ac	73 c at a Il	c tg e Cy	t ca s Hi 5	c cc s Pr	t ct o Le	g ag u Ar	a ta g Ty	ic ac vr Th	r As	ac at sp Il	c at e Me	g ac t Th	t co ir Pr 15	et cgt o Arg	49
ctg Leu	tgt Cys	ggt Gly	ctg Leu 20	ctg Leu	gtt Val	tca Ser	ctt Leu	tcc Ser 25	ctg Leu	tcc Ser	att Ile	Cys	tcc Ser 30	gcg Ala	gat Asp	97
gcc Ala	ctg Leu	ctc Leu 35	cac His	agc Ser	ctc Leu	atg Met	ctg Leu 40	ctg Leu	cag Gln	ctg Leu	tcc Ser	ttc Phe 45	tgc Cys	aca Thr	gac Asp	145
ctt Leu	gaa Glu 50	atc Ile	tcc Ser	ctt Leu	ttc Phe	ttc Phe 55	tgt Cys	gaa Glu	gtc Val	gtt Val	cag Gln 60	gtc Val	gtc Val	aag Lys	ctc Leu	193
gcg Ala 65	tgc Cys	tcc Ser	gat Asp	acc Thr	ctc Leu 70	gtc Val	aac Asn	aac Asn	ctt Leu	ctg Leu 75	atc Ile	tat Tyr	ttt Phe	gca Ala	gct Ala 80	241
tgc Cys	acc Thr	ttg Leu	ggt Gly	ggc Gly 85	att Ile	cct Pro	ctg Leu	tct Ser	ggc Gly 90	atc Ile	att Ile	ttt Phe	tct Ser	tac Tyr 95	act Thr	289
caa Gln	ata Ile	gcc Ala	acc Thr 100	tcc Ser	att Ile	ttg Leu	aaa Lys	atg Met 105	ccg Pro	tca Ser	tcg Ser	ggc Gly	aga Arg 110	aag Lys	tat Tyr	337
aaa Lys	gcc Ala	ttt Phe 115	tcc Ser	acc Thr	tgt Cys	Gl <sup>à</sup> aaa	tct Ser 120	cac His	ctg Leu	tca Ser	gtt Val	gtt Val 125	tcc Ser	ctg Leu	ttc Phe	385
tat Tyr	999 Gly 130	Thr	ggt Gly	ttg Leu	gly ggg	gtg Val 135	tac Tyr	atc Ile	agt Ser	tct Ser	gca Ala 140	gtt Val	tct Ser	gac Asp	tct Ser	433
t.ca	agg	agg	act	aca	qta	gct	tca	gtg	atg	tac	act	gtg	gtc	act	ccc	481

Ser Arg Arg Thr Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro 150 155 486 tgt tg Cys <210> 274 <211> 161 <212> PRT <213> Eulemur rubriventer <220> <221> misc\_feature <222> (1)..(486)
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Cys

<210> 275 <211> 487

<212 <213		ONA Eulen	nur r	ubri	vent	er										
<220 <221 <222 <223	.> n	nisc_ (1) Taxor	(487	')	; ge	ne =	ERU	J168;	Acc	essi	on D	DBJ/	'EMBI	⊿/Gen	ıBank =	AF179791
<220 <221 <222 <223	.> ( !>	CDS (2) Produ			acto	ory r	ecep	otor								
<400 t gt Va 1	a a	275 cc at la Il	c to	gt ca /s Hi 5	c co s Pr	ct ct	g ac u Th	a ta ir Ty	ic ac r Th	r As	ıc at sp Il	c at e Me	g ac et Th	et co nr Pr 15	ct cgt co Arg	49
ctg Leu	tgt Cys	ggt Gly	ctg Leu 20	ctg Leu	gtt Val	tca Ser	ctt Leu	tcc Ser 25	ctg Leu	tcc Ser	att Ile	tgc Cys	tcc Ser 30	gcg Ala	gat Asp	97
gcc Ala	ctg Leu	ctc Leu 35	cac His	agc Ser	ctc Leu	atg Met	ctg Leu 40	ctg Leu	cag Gln	ctg Leu	tcc Ser	ttc Phe 45	tgc Cys	aca Thr	gac Asp	145
ctt Leu	gaa Glu 50	atc Ile	tcc Ser	ctt Leu	ttc Phe	ttc Phe 55	tgt Cys	gaa Glu	gtc Val	gtt Val	cag Gln 60	gtc Val	gtc Val	aag Lys	ctc Leu	193
gcg Ala 65	tgc Cys	tcc Ser	gat Asp	acc Thr	ctc Leu 70	gtc Val	aac Asn	aac Asn	ctt Leu	ctg Leu 75	atc Ile	tat Tyr	ttt Phe	gca Ala	gct Ala 80	241
tgc Cys	acc Thr	ttg Leu	ggt Gly	ggc Gly 85	att Ile	cct Pro	ctg Leu	tct Ser	ggc Gly 90	atc Ile	att Ile	ttt Phe	tct Ser	tac Tyr 95	act Thr	289
caa Gln	ata Ile	gcc Ala	acc Thr 100	tcc Ser	att Ile	ttg Leu	aaa Lys	atg Met 105	ccg Pro	tca Ser	tcg Ser	ggc Gly	aga Arg 110	aag Lys	tat Tyr	337
aaa Lys	gcc Ala	ttt Phe 115	tcc Ser	gcc Ala	tgt Cys	ggg Gly	tct Ser 120	cac His	ctg Leu	tca Ser	gtt Val	gtt Val 125	tcc Ser	ctg Leu	ttc Phe	385
tat Tyr	999 Gly 130	aca Thr	ggt Gly	ttg Leu	gly aaa	gtg Val 135	tac Tyr	atc Ile	agt Ser	tct Ser	gca Ala 140	gtt Val	tct Ser	gac Asp	tct Ser	433
tca Ser 145	agg Arg	agg Arg	act Thr	gcg Ala	gtg Val 150	Ala	tca Ser	gtg Val	atg Met	tac Tyr 155	act Thr	gtg Val	gtc Val	act Thr	ccc Pro 160	481
	ttg Leu															487
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Val Ala Ile Cys His Pro Leu Thr Tyr Thr Asp Ile Met Thr Pro Arg 10

Leu Cys Gly Leu Leu Val Ser Leu Ser Leu Ser Ile Cys Ser Ala Asp

Ala Leu Leu His Ser Leu Met Leu Leu Gln Leu Ser Phe Cys Thr Asp

Leu Glu Ile Ser Leu Phe Phe Cys Glu Val Val Gln Val Val Lys Leu 50

Ala Cys Ser Asp Thr Leu Val Asn Asn Leu Leu Ile Tyr Phe Ala Ala

Cys Thr Leu Gly Gly Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr

Gln Ile Ala Thr Ser Ile Leu Lys Met Pro Ser Ser Gly Arg Lys Tyr 100

Lys Ala Phe Ser Ala Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 120 115

Tyr Gly Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Ser Asp Ser 135 130

Ser Arg Arg Thr Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro 155 150

Val Leu

<210> 277

<211> 486

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(1)..(486)

<223> Taxon = 9546; gene = MSY172; Accession DDBJ/EMBL/GenBank = AF179792

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(1)..(486) <222>

<223> Product = olfactory receptor

<400> 277

cct gcc atc tgc cag cca ctc agg tac cgc gtg ctc atg aac cac cgg

48

Pro 1	Ala	Ile	Cys	Gln 5	Pro	Leu	Arg	Tyr	Arg 10	Val	Leu	Met	Asn	His 15	Arg	
ctc Leu	tgt Cys	gtg Val	ctg Leu 20	ctg Leu	gtg Val	gga Gly	gct Ala	gcc Ala 25	tgg Trp	gtc Val	ctc Leu	tgc Cys	ctc Leu 30	ctc Leu	aag Lys	96
tcg Ser	gtg Val	act Thr 35	gag Glu	aca Thr	gtc Val	att Ile	gcc Ala 40	atg Met	agg Arg	ctg Leu	ccc Pro	ttc Phe 45	tgt Cys	gly	cac His	144
cac His	gtg Val 50	gtc Val	agt Ser	cac His	ttc Phe	acc Thr 55	tgc Cys	gag Glu	atc Ile	ctg Leu	gcg Ala 60	gtg Val	ctg Leu	aag Lys	ctg Leu	192
acg Thr 65	tgc Cys	ggt Gly	aac Asn	aca Thr	tcg Ser 70	gtc Val	agc Ser	gag Glu	gtc Val	ttc Phe 75	ctg Leu	ctg Leu	gtg Val	ggc Gly	tcc Ser 80	240
atc Ile	ctg Leu	ctg Leu	ctg Leu	cct Pro 85	gtg Val	ccc Pro	ctg Leu	gca Ala	ttc Phe 90	att Ile	tgc Cys	ctg Leu	tcc Ser	tac Tyr 95	ttg Leu	288
ctc Leu	atc Ile	ctg Leu	gcc Ala 100	acc Thr	atc Ile	ctg Leu	agg Arg	gtg Val 105	ccc Pro	tca Ser	gct Ala	gct Ala	999 Gly 110	tgc Cys	cgc Arg	336
aaa Lys	gcc Ala	ttc Phe 115	tcc Ser	acc Thr	tgc Cys	tca Ser	gca Ala 120	cac His	ctg Leu	gct Ala	gtg Val	gtg Val 125	ctg Leu	ctt Leu	ttc Phe	384
tac Tyr	agc Ser 130	Thr	atc Ile	atc Ile	ttc Phe	acg Thr 135	tac Tyr	atg Met	aag Lys	ccc Pro	aag Lys 140	agc Ser	aag Lys	gaa Glu	gcc Ala	432
cac His 145	atc Ile	tct Ser	gat Asp	gag Glu	gtc Val 150	Phe	aca Thr	gtc Val	ctc Leu	tac Tyr 155	Ala	atg Met	gtc Val	aca Thr	ccc Pro 160	480
_	ttg Leu															486
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Pro 1	Ala	ı Ile	: Cys	Glr 5	n Pro	Leu	a Arg	ј Туг	Arg 10	y Val	. Leu	ı Met	. Asr	His	Arg	
Leu	суя	s Val	. Let 20	ı Lev	ı Val	. Gly	/ Ala	a Ala 25	a Trp	val	. Lev	ı Cys	Lev 30	ı Lev	Lys	
Ser	· Val	l Thi	: Glı	ı Thi	va.	l Ile	e Ala 40	a Met	t Arg	g Let	ı Pro	Phe 45	е Суя	s Gly	/ His	

His Val Val Ser His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu

Thr Cys Gly Asn Thr Ser Val Ser Glu Val Phe Leu Leu Val Gly Ser

Ile Leu Leu Pro Val Pro Leu Ala Phe Ile Cys Leu Ser Tyr Leu

Leu Ile Leu Ala Thr Ile Leu Arg Val Pro Ser Ala Ala Gly Cys Arg 100 105

Lys Ala Phe Ser Thr Cys Ser Ala His Leu Ala Val Val Leu Leu Phe 120

Tyr Ser Thr Ile Ile Phe Thr Tyr Met Lys Pro Lys Ser Lys Glu Ala 140

His Ile Ser Asp Glu Val Phe Thr Val Leu Tyr Ala Met Val Thr Pro

Met Leu

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<212> DNA

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<220>

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<210> 280

atgtagatt

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<223> product = olfactory receptor
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                                                                          49
  Val Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Ser Gln Pro
                                       1.0
atg tgt gga ttc ctg atg ggg gtg gct ggg att ctg gga ttt gtg cat
Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His
                                                                          97
            20
gga ggg atc cag act ttg ttc ata gcc cac tta cca ttc tgt ggc cct
                                                                         145
Gly Gly Ile Gln Thr Leu Phe Ile Ala His Leu Pro Phe Cys Gly Pro
        35
aat gtc atc gac cac ttt atg tgt gat tta gta cct ctt cta gag ctg
                                                                         193
Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu
                         55
gee tge aca gae act cae ace ttg ggg eet etg ata get gee aac agt
                                                                         241
Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser
                                                                         289
gga tca ttg tgt ttc ctc att ttt tcc atg ctg gtt gct tcc tat gtc
Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val
                                      90
                 85
                                                                         337
atc atc ctg tgc tcc cta agg act cat atc tct gaa ggg cgt cac aaa
Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys
                                                       110
             100
gtt ctg tct agt tgt acc tct cat atc ttt gtt gtc atc tta ttc ttt
                                                                         385
Val Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe
                                                   125
                              120
gtc cct tgt tca tac ctg tat cta aga cct cta acc tcc ttc ttc ccc
                                                                         433
Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Phe Pro
     130
act gac aaa gct gtg act gtg ttt tgc acc cta ttt aca cct atg ttg
                                                                         481
Thr Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu
145
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       160
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Val	Ala	Ile	Cys	Lys	Pro	Leu	His	Tyr	Ala	Thr	Ile	Met	Ser	Gln	Pro
1				5					10					15	

Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His 20

Gly Gly Ile Gln Thr Leu Phe Ile Ala His Leu Pro Phe Cys Gly Pro

Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu

Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser

Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val 95 85

Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys 100

Val Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe 115

Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Phe Pro 130

Thr Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu 150 155

282 <210>

<400> 281

402 <211>

<212> DNA

<213> Macaca sylvanus

<220>

misc\_feature <221>

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<400> 282

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      487
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      DNA
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       Taxon = 9546; gene = MSY176; Accession DDBJ/EMBL/GenBank = AF179796
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<222>
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<223> Product = olfactory receptor
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                                                                             49
  Val Ala Ile Cys Asn Pro Leu Leu Tyr Ala Leu Val Val Ser Pro Lys
gta tgt cgt ctg ctg gtg tcc ctc aca tac ctt cag agt ctt atc aca
                                                                             97
Val Cys Arg Leu Leu Val Ser Leu Thr Tyr Leu Gln Ser Leu Ile Thr
gcc ctt act gtc tct tcc tgt gtg ttc tct gtg tca tac tgt tct tcc
Ala Leu Thr Val Ser Ser Cys Val Phe Ser Val Ser Tyr Cys Ser Ser
                                                                            145
         35
                                                                             193
aac atc atc aac cat ttt tac tgt gac gat gtc cct ttg cta gca ttg
Asn Ile Ile Asn His Phe Tyr Cys Asp Asp Val Pro Leu Leu Ala Leu
                           55
teg tgt tet gat ace tae att eea gaa aca gea gtg ttt ate ttt tea
                                                                             241
Ser Cys Ser Asp Thr Tyr Ile Pro Glu Thr Ala Val Phe Ile Phe Ser
65
                                                                             289
ggg acc aat ttg ttt ttc tcc atg acc gtt gtt ctg ata tcc tac ttc
Gly Thr Asn Leu Phe Phe Ser Met Thr Val Val Leu Ile Ser Tyr Phe
                                        90
aac att gtt att acc att ttg agg ata cgt tcc tca gaa gga cga caa
                                                                             337
Asn Ile Val Ile Thr Ile Leu Arg Ile Arg Ser Ser Glu Gly Arg Gln
                                    105
aaa gcc ttt tcc acg tgt gct tct cac atg ata gct gtg gtt gtg ttc
Lys Ala Phe Ser Thr Cys Ala Ser His Met Ile Ala Val Val Phe
                                                                             385
tat ggg act ctc ctt ttc atg tat ttg caa cca agg agt aat cac tca
                                                                             433
 Tyr Gly Thr Leu Leu Phe Met Tyr Leu Gln Pro Arg Ser Asn His Ser
                           135
 tta gat act gac aaa atg gcc tcg gtc ttc tac acc ctg atc ata cct
                                                                             481
 Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Ile Ile Pro
                                                                   160
                       150
 145
                                                                             487
 atg ttg
 Met Leu
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<220>

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Val Cys Arg Leu Leu Val Ser Leu Thr Tyr Leu Gln Ser Leu Ile Thr
             20
Ala Leu Thr Val Ser Ser Cys Val Phe Ser Val Ser Tyr Cys Ser Ser
Asn Ile Ile Asn His Phe Tyr Cys Asp Asp Val Pro Leu Leu Ala Leu
Ser Cys Ser Asp Thr Tyr Ile Pro Glu Thr Ala Val Phe Ile Phe Ser
Gly Thr Asn Leu Phe Phe Ser Met Thr Val Val Leu Ile Ser Tyr Phe
                                                            95
Asn Ile Val Ile Thr Ile Leu Arg Ile Arg Ser Ser Glu Gly Arg Gln
Lys Ala Phe Ser Thr Cys Ala Ser His Met Ile Ala Val Val Phe
         115
Tyr Gly Thr Leu Leu Phe Met Tyr Leu Gln Pro Arg Ser Asn His Ser
     130
Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Ile Ile Pro
                     150
 Met Leu
 <210> 285
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 <223> Taxon = 9546; gene = MSY177; Accession DDBJ/EMBL/GenBank = AF179797
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<222> (2)..(487)
<223> Product = olfactory receptor
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  Val Ala Ile Cys His Pro Leu His Tyr Ala Ile Ile Met Gly Gln Ser
cag tgt gtc acg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt
                                                                              97
Gln Cys Val Thr Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
             20
gct ctt ttg cac act ctc ctc ctg gcc tgg ctt tcc ttc tgt gct gat
                                                                             145
Ala Leu Leu His Thr Leu Leu Leu Ala Trp Leu Ser Phe Cys Ala Asp
                                                                             193
cac atc atc cct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ttg
His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
                           55
tee tge tea gae ace tee etc aat eag tta gea ate ttt aca gea gga
                                                                             241
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
                                                                              289
ttg aca gcc att atg ctt cca ttc ctg tgt atc ctg gtt tct tat ggt
Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
                  85
                                                                              337
cac act gca gtc acc atc ctc cag att ccc tct act aat ggc ata tgc
His Thr Ala Val Thr Ile Leu Gln Ile Pro Ser Thr Asn Gly Ile Cys
              100
aaa gcc ttg tcc act tgt gga tcc cac ctc tca gca gtg act ctc tat
                                                                              385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Ala Val Thr Leu Tyr
                                                      125
tat ggg acc att att ggt ctc tat ttt ctt ccc cca tcc agc aac act
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
                                                                              433
                           135
     130
aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
                       150
                                                                              487
 atg ttg
Met Leu
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 Val Ala Ile Cys His Pro Leu His Tyr Ala Ile Ile Met Gly Gln Ser
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Gln Cys Val Thr Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
                                  25
            20
Ala Leu Leu His Thr Leu Leu Leu Ala Trp Leu Ser Phe Cys Ala Asp
His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
                                      90
His Thr Ala Val Thr Ile Leu Gln Ile Pro Ser Thr Asn Gly Ile Cys
                                 105
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Ala Val Thr Leu Tyr
                              120
        115
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
                          135
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
                                           155
                      150
Met Leu
<210> 287
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                                                                           49
  Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
ctc tgt ctc gcc ctg gtg gcg ctg tcc tgg gta ctg acc acc ttc cat
Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
                                                                           97
```

145

25

gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp

35 40 aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg 193 Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu 55 gcc tgc tct gac act caa gtt aat gaa ttg gcg ata ttt atc acg gga 241 Ala Cys Ser Asp Thr Gln Val Asn Glu Leu Ala Ile Phe Ile Thr Gly 75 70 ggg ctg att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala 289 90 cgg att gtc tcc tcc atc ctc aag gtc cct tcg tct aag ggt atc tgc Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys 337 100 385 aag goe tte tet act tgt gge tee cae ete tet gtg gtg tea etg tte Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 120 433 tat ggg acc gtt att ggt ctc tac ttc tgc cca tca gct aat agt tct Tyr Gly Thr Val Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser 135 act cta aag gag act gtc atg gct atg atg tac act gtg gtg acc ccc Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro 481 155 487 atg ctg Met Leu <210> 288 <211> 162 <212> PRT <213> Macaca sylvanus <220> <221> misc\_feature (1)..(487) <222> Taxon = 9546; gene = MSY178; Accession DDBJ/EMBL/GenBank = AF179798 <400> 288 Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met 10 Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His 20 Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp 35

Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu 50 55 60

Ala Cys Ser Asp Thr Gln Val Asn Glu Leu Ala Ile Phe Ile Thr Gly 65 70 75 80

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Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
                                105
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
Tyr Gly Thr Val Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser
Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
                    150
Met Leu
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       484
       DNA
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<222> (2)..(484)
<223> Product = olfactory receptor
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                                                                       49
  Cys Ala Ile Cys Cys Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys
                                                                       97
 ctc tgt atc tta ctc ctt tcc ttg tgt tgg gtc tta tct gtg ctc tat
Leu Cys Ile Leu Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr
             20
 ggc ctc ata cac acc ttc ctc atg acc acg gtg acc ttc tgt ggg tca
                                                                      145
 Gly Leu Ile His Thr Phe Leu Met Thr Thr Val Thr Phe Cys Gly Ser
 cga aaa atc cac tac atc ttc tgt gag atg tat gta ttg ctg agg ctg
                                                                      193
 Arg Lys Ile His Tyr Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Leu
                                             60
 gca tgt tcc gac act cag att aat cac aca gtg ctg att gcc aca ggc
                                                                       241
 Ala Cys Ser Asp Thr Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly
                     70
 tgc ttt atc ttc ctc att ccc ttt gga ttc atg atc att tcc tat gtg
                                                                       289
 Cys Phe Ile Phe Leu Ile Pro Phe Gly Phe Met Ile Ile Ser Tyr Val
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337

90

ttg att gtc aga gcc atc ctc aga ata ccc tca gtc tct aag aaa tac

Leu Ile		Arg <i>l</i>	Ala	Ile	Leu	Arg	Ile 105	Pro	Ser	Val	Ser	Lys 110	Lys	Tyr	
aaa gcc Lys Ala	ttc t Phe S	cc a Ser :	act Thr	tgt Cys	gcc Ala	tcc Ser 120	cat His	ttg Leu	ggt Gly	gta Val	gtc Val 125	tcc Ser	ctc Leu	ttc Phe	385
tat ggg Tyr Gly 130	Thr I	ctt ( Leu (	tgt Cys	atg Met	gta Val 135	tac Tyr	ctg Leu	aag Lys	ccc Pro	ctc Leu 140	cat His	acc Thr	tac Tyr	tct Ser	433
gtg aag Val Lys 145	gac t Asp £	tca ( Ser '	gta Val	gcc Ala 150	aca Thr	gtg Val	atg Met	tat Tyr	gcg Ala 155	gtg Val	gtg Val	aca Thr	ccc Pro	atg Met 160	481
atg Met							•								484
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Leu Cys		Leu 20	Leu	Leu	Ser	Leu	Cys 25	Trp	Val	Leu	Ser	Val 30	Leu	Tyr	
Gly Le	ı Ile 35	His	Thr	Phe	Leu	Met 40	Thr	Thr	Val	Thr	Phe 45	Cys	Gly	Ser	
Arg Ly: 50	s Ile	His	Tyr	Ile	Phe 55	Cys	Glu	Met	Tyr	Val 60	Leu	Leu	Arg	Leu	
Ala Cys 65	s Ser	Asp	Thr	Gln 70	Ile	Asn	His	Thr	Val	Leu	Ile	Ala	Thr	Gly 80	
Cys Pho	e Ile	Phe	Leu 85	Ile	Pro	Phe	Gly	Phe	. Met	Ile	Ile	. Ser	Tyr 95	Val	
Leu Il	e Val	Arg 100	Ala	Ile	Leu	Arg	Ile 105		Ser	· Val	Ser	Lys 110	Lys	Tyr	
Lys Al	a Phe 115	Ser	Thr	Cys	Ala	Ser 120		ș Lev	ı Gly	v Val	Va]	. Ser	Leu	Phe	
Tyr Gl 13		Leu	Cys	Met	. Val 135		: Le	ı Lys		140	His	3 Thr	туг	: Ser	

145

Met

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= AF179800
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cttagtggct gtatcttgaa ttctgtcttg tgccagctcc ctctctcaca cccttctcct
                                                                     120
gacccagetg tetttetgtg etgegaacae catececcae atettetgtg acettgetge
                                                                     180
cctgctcaag ctgtcctggt cagatatctt cctcaatgag ctggtcatgt tcacagtagg
                                                                     240
ggtggtggtc attaccctgc cattcatgtg tatcctggta tcatatggct acactggggc
                                                                     300
                                                                     360
caccatectg agggteeett caaccaaagg gatecacaaa geattgteea catgtgeete
ccatctctct gtggtttctc tctattatgg gtcaatattt ggccagtaac atttcccaac
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tgtaagcagt tctattgaca aggatgttac tgtggctctc atgtacatcg tggtcacacc
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cgtgttg
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cttagtggct gtatcttgaa ttctgtcttg tgccagctcc ctctctcaca cccttctcct
gacccagctg tctttctgtg ctgcgaacac catcccccac atcttctgtg accttgctgc
cctgctcaag ctgtcctggt cagatatctc cctcaatgag ctggtcatgt tcacagtagg
                                                                      240
ggtggtggtc attaccctgc cattcatgtg tatcctggta tcatatggct acactggggc
                                                                      300
caccatcctg agggtccctt caaccaaagg gatccacaaa gcattgtcca catgtgcctc
                                                                      360
ccatctctct gtggtttctc tctattatgg gtcaatattt ggccagtaac atttcccaac
                                                                      420
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250

Val Lys Asp Ser Val Ala Thr Val Met Tyr Ala Val Val Thr Pro Met

155

tgtaa	agca	gt t	ctati	tgac	a ag	gatg	ttac	tgt	ggct	ctc .	atgt	acat	cg t	ggtc	acacc	480	
cgtgttg														487			
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gtg Val	tgt Cys	acc Thr	tta Leu 20	tta Leu	gtc Val	ctc Leu	tgc Cys	agt Ser 25	tgg Trp	gtg Val	gct Ala	ggc Gly	ttg Leu 30	atg Met	atc Ile	97	
att Ile	gtt Val	cca Pro 35	cca Pro	ctg Leu	agc Ser	tta Leu	ggc Gly 40	ctc Leu	cag Gln	ctc Leu	gaa Glu	ttc Phe 45	tgt Cys	ggc Gly	tcc Ser	145	
aat Asn	gcc Ala 50	att Ile	gat Asp	cat His	ttt Phe	agc Ser 55	tgt Cys	gat Asp	gca Ala	ggt Gly	cct Pro 60	ctc Leu	cta Leu	aag Lys	atc Ile	193	
tca Ser 65	tac	tca Ser	gac Asp	aca Thr	tgg Trp 70	gta Val	ata Ile	gaa Glu	cag Gln	ata Ile 75	gtt Val	ata Ile	ctt Leu	atg Met	gct Ala 80	241	
gta Val	ttt Phe	gca Ala	ctc Leu	att Ile 85	atc Ile	acc Thr	cta Leu	gtt Val	tgt Cys 90	gtg Val	att Ile	ctg Leu	tcc Ser	tac Tyr 95	ttg Leu	289	
tac Tyr	ata Ile	gtc Val	aga Arg 100	aca Thr	att Ile	ctg Leu	agg Arg	ttc Phe 105	cct Pro	tct Ser	gtt Val	cag Gln	caa Gln 110	agg Arg	aaa Lys	337	
aag Lys	gcc Ala	ttt Phe 115	Ser	acc Thr	tgt Cys	tca Ser	tcc Ser 120	His	atg Met	att Ile	gtg Val	gtt Val 125	tcc Ser	att Ile	gcc Ala	385	
tat Tyr	gga Gly 130	agc Ser	tgc Cys	atc Ile	ttc Phe	gtc Val 135	Tyr	atc Ile	aag Lys	ccc Pro	tct Ser 140	gca Ala	aaa Lys	gat Asp	gaa Glu	433	
gtg Val 145	gcc Ala	ata Ile	aat Asn	aaa Lys	gga Gly 150	Val	tca Ser	gtt Val	ctt Leu	act Thr 155	Thr	tct Ser	gtt Val	gca Ala	ccc Pro 160	481	
_	ttg Leu															487	,

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Ile Val Pro Pro Leu Ser Leu Gly Leu Gln Leu Glu Phe Cys Gly Ser
Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile
Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Ile Val Ile Leu Met Ala
Val Phe Ala Leu Ile Ile Thr Leu Val Cys Val Ile Leu Ser Tyr Leu
Tyr Ile Val Arg Thr Ile Leu Arg Phe Pro Ser Val Gln Gln Arg Lys
            100
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala
                            120
Tyr Gly Ser Cys Ile Phe Val Tyr Ile Lys Pro Ser Ala Lys Asp Glu
Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Thr Ser Val Ala Pro
                                        155
                    150
Leu Leu
<210> 295
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<223> Taxon = 9483; gene = CJA169; Accession DDBJ/EMBL/GenBank = AF179803

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 Val Ala Ile Cys Arg Pro Leu Tyr Tyr Ser Thr Val Met Ser Pro Gln
gtc tgt gcc cta atc ctt gca ttg tgc tgg gtc ctc acc aat gtt gtt
                                                                          97
Val Cys Ala Leu Ile Leu Ala Leu Cys Trp Val Leu Thr Asn Val Val
                                                                         145
gcc ctg act cac aca ctc ctc atg gct cga ctg tcc ttc tgt gtg act
Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr
                                                                         193
ggg gaa ata gct cac ttt ttc tgt gac atc act cct gtc ctg aag cta
Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
tca tgt tct gac acc cac atc aac gag atg atg gtt ttt gtc ttg gga
Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
                                                                         241
                     70
ggc aca gta ctc att gtc ccc ttt ata tgc att gtc acc tcc tac atc
                                                                         289
Gly Thr Val Leu Ile Val Pro Phe Ile Cys Ile Val Thr Ser Tyr Ile
                 85
                                                                         337
cac att gtg cct gct atc ctg agg gtc cga acc tgt ggt ggg gcg ggc
His Ile Val Pro Ala Ile Leu Arg Val Arg Thr Cys Gly Gly Ala Gly
                                  105
                                                                         385
aag gcc ttt tcc acc tgc agt tcc cac ctc tgc att gtt tgt ata ttc
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Ile Phe
                             120
                                                  125
                                                                         433
tat ggg acc ctc ttc agt gcc tac ctg tgt cct ccc tct att gcc tct
Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser
gaa gag aag gac att gca gca gct gca ctg tat acc ata gtg act ccc
                                                                         481
Glu Glu Lys Asp Ile Ala Ala Ala Ala Leu Tyr Thr Ile Val Thr Pro
                     150
                                                                         487
atg ttg
Met Leu
<210> 296
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<222>
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Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr
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Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu

Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly 75

Gly Thr Val Leu Ile Val Pro Phe Ile Cys Ile Val Thr Ser Tyr Ile

His Ile Val Pro Ala Ile Leu Arg Val Arg Thr Cys Gly Gly Ala Gly 110

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Ile Phe 120 115

Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser 130

Glu Glu Lys Asp Ile Ala Ala Ala Ala Leu Tyr Thr Ile Val Thr Pro 150

Met Leu

20

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<210> 297
<211> 486
<212> DNA
<213> Callithrix jacchus
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<223> Product = olfactory receptor
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Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg
ctg tgt gga ctg ctg gtt ctg gca tcc tgg atc ctg agt gcc ctg aat
                                                                         96
Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
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3.0

tcc tca tta Ser Ser Leu 35	caa acc Gln Thr	tta ata Leu Ile	gtg ct Val Le 40	g cgg au Arg	ctt Leu	tcc Ser	ttc Phe 45	tgc Cys	aca Thr	gac Asp	144
ttg gaa atc Leu Glu Ile 50	ccc cgc Pro Arg	ttt ttc Phe Phe 55	tgc ga Cys Gl	a ctt Lu Leu	Asn	cag Gln 60	gtc Val	atc Ile	cac His	ctt Leu	192
gcc tgt tct Ala Cys Ser 65	gac act Asp Thr	ttt ctt Phe Leu 70	aat ga Asn As	at gtg sp Val	gtg Val 75	atg Met	tat Tyr	ttg Leu	gcc Ala	gct Ala 80	240
gtg ctg ctg Val Leu Leu	ggg ggt Gly Gly 85	ggt ccc Gly Pro	ctt go Leu Al	ca ggg la Gly 90	att Ile	ctt Leu	tac Tyr	tct Ser	tac Tyr 95	tct Ser	288
aag ata gtt Lys Ile Val	tcc tcc Ser Ser 100	ata cgt Ile Arg	Ala I	tc tca le Ser 05	tca Ser	gct Ala	cag Gln	999 Gly 110	aag Lys	tac Tyr	336
aag gca ttt Lys Ala Phe 115	tcc acc Ser Thr	tgt gta Cys Val	tct ca Ser H 120	ac atc is Ile	tta Leu	att Ile	gtc Val 125	tcc Ser	tta Leu	ttt Phe	384
tat ggt aca Tyr Gly Thr 130	ctc cta Leu Leu	ggt gtg Gly Val 135	Tyr L	tt agt eu Ser	tct Ser	gct Ala 140	gca Ala	act Thr	ggc Gly	aac Asn	432
tca cat tca Ser His Ser 145	aga gct Arg Ala	gca gcc Ala Ala 150	tcg g Ser V	tg atg al Met	tac Tyr 155	act Thr	gtg Val	gtc Val	acc Thr	ccc Pro 160	480
atg ctg Met Leu											486
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Leu Cys Gly	y Leu Le 20	u Val Le	ı Ala S	Ser Trp 25	o Ile	Leu	. Ser	30	ı Let	ı Asn	
Ser Ser Let 35	ı Gln Th	r Leu Ilo	e Val I 40	Leu Arg	g Leu	Ser	Phe 45	e Cys	s Thi	qaA c	
Leu Glu Ile 50	e Pro Ar	g Phe Ph 55	e Cys (	Glu Le	u Asn	Glr 60	ı Val	l Ile	e Hi	s Leu	
Ala Cys Se	r Asp Th	r Phe Le	u Asn	Asp Va		. Met	ту:	r Le	u Al	a Ala	

Val Leu Cly Cly Cly Pro Leu Ala Cly Ile Leu Tyr Ser Tyr Ser 85 90 95

70

Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gl<br/>n Gly Lys Tyr 100 105 110

Lys Ala Phe Ser Thr Cys Val Ser His Ile Leu Ile Val Ser Leu Phe 115 120 125

Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn 130 135 140

Ser His Ser Arg Ala Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro 145 150 155 160

Met Leu

<210> 299 <211> 487 <212> DNA <213> Callithrix jacchus <220> misc\_feature <221> <222> (1)...(487)Taxon = 9483; gene = CJA171; Accession DDBJ/EMBL/GenBank = AF179805 <223> <220> <221> CDS (2)..(487) <222> <223> Product = olfactory receptor <400> 299 c gtg gcc atc tgt aac cca ctg ttg tac atg gtc acc atg tct ccc cag 49 Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln 5 gtg tgc ttg ctc ctt ttg ttg ggt gtc tat ggg atg ggg gct ttg ggg 97 Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Ala Leu Gly gct gtg gct cat atg gga aac ata atg ttt atg acc ttt tgt gca gaa 145 Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ala Glu acc ctt gtc aat cac tac atg tgt gac atc ctt ccc ctc ctt gag ctc 193 Thr Leu Val Asn His Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu 50 tcc tgc aac agc tct tac ata aat ttg ctg ttg gtt ttt att att gtg Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val

90

acc att ggc att ggg gtg ccc att gtc acc att ttt atc tct tat ggt Thr Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly

70

85

ttt att ctt tcc agc att ctc cac att agt tct gct gag ggc agg tct  Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Ala Glu Gly Arg Ser  100 105 110	
aaa gcc ttc agt acc tgc agc tcc cac ata gtt gtg gta ttg ctt ttc 385 Lys Ala Phe Ser Thr Cys Ser Ser His Ile Val Val Val Leu Leu Phe 115 120 125	
ttt ggg tca gga gct ttt atg tac ctc aaa cca cct tct att cta ccc Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro 130 135 140	
ctg gac cag ggg aaa gtg tcc tcc att ttt tat act gcg gtg gtg ccc Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro 145 150 155 160	
atg ttt Met Phe 487	
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Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln 1 5 10 15	
Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Ala Leu Gly 20 25 30	
Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ala Glu 35 40 45	
Thr Leu Val Asn His Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu 50 55 60	
Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val 65 70 75 80	
Thr Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly 85 90 95	
Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Ala Glu Gly Arg Ser 100 105 110	
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Val Val Leu Leu Phe 115 120 125	

Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro 130 135 140

Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro 145 150 155 160

Met Phe

<210><211><212><213>	301 487 DNA Calli	thri	х ja	cchu	.s										
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agc tg Ser Cy	c acc	cta Leu 20	atg Met	ttg Leu	ggc Gly	tgc Cys	tta Leu 25	tgg Trp	acc Thr	act Thr	gcc Ala	agc Ser 30	ctc Leu	cat His	97
gcc ct Ala Le	t ctg u Leu 35	cac His	acc Thr	ctt Leu	ctc Leu	ttg Leu 40	gcc Ala	cgg Arg	ctg Leu	gac Asp	ttc Phe 45	tgt Cys	gcc Ala	agc Ser	145
aat gt Asn Va 50	ıl Ile	ccc Pro	tac Tyr	ttc Phe	ttc Phe 55	tgt Cys	gac Asp	ctc Leu	gtt Val	ccc Pro 60	ctg Leu	ctc Leu	cag Gln	ctc Leu	193
tcc to Ser Cy 65	jt tct 's Ser	gac Asp	acc Thr	cga Arg 70	ctc Leu	aac Asn	cag Gln	ctc Leu	atg Met 75	att Ile	gtg Val	ctg Leu	gtg Val	999 61y 80	241
ggc ct Gly Le	g atc eu Ile	atc Ile	ctc Leu 85	ctg Leu	ccc Pro	ttc Phe	ctt Leu	ggc Gly 90	att Ile	ctc Leu	ggt Gly	tcc Ser	tac Tyr 95	aca Thr	289
tgc at Cys Il	t gca le Ala	gct Ala 100	gca Ala	gtg Val	ctc Leu	aga Arg	gtc Val 105	ccc Pro	tct Ser	gcc Ala	agg Arg	ggt Gly 110	acg Thr	tgg Trp	337
aag go Lys Al	ec ttt la Phe 115	Ser	acc Thr	tgt Cys	ggc Gly	tcc Ser 120	cac His	ctg Leu	acc Thr	atg Met	gtc Val 125	atc Ile	ctc Leu	ttc Phe	385
tat go Tyr G	gc acc ly Thr 30	atc Ile	tca Ser	ggg Gly	gtc Val 135	tac Tyr	ctg Leu	agg Arg	ccc Pro	tca Ser 140	tcc Ser	tcc Ser	cac His	tcc Ser	433
aca ga Thr A	ac aag sp Lys	gac Asp	tca Ser	cta Leu	gcc Ala	tca Ser	gtg Val	atg Met	tac Tyr	atg Met	gta Val	gtg Val	acc Thr	ccc Pro	481

<210> 302 <211> 162

<212> PRT

<213> Callithrix jacchus

<220>

<221> misc\_feature

<222> (1)..(487)

<223> Taxon = 9483; gene = CJA196; Accession DDBJ/EMBL/GenBank = AF179806

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Ser Cys Thr Leu Met Leu Gly Cys Leu Trp Thr Thr Ala Ser Leu His 20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Asp Phe Cys Ala Ser 35 40 45

Asn Val Ile Pro Tyr Phe Phe Cys Asp Leu Val Pro Leu Leu Gln Leu 50 55 60

Ser Cys Ser Asp Thr Arg Leu Asn Gln Leu Met Ile Val Leu Val Gly 65 70 75 80

Gly Leu Ile Ile Leu Leu Pro Phe Leu Gly Ile Leu Gly Ser Tyr Thr 85 90 95

Cys Ile Ala Ala Ala Val Leu Arg Val Pro Ser Ala Arg Gly Thr Trp

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Met Val Ile Leu Phe 115 120 125

Tyr Gly Thr Ile Ser Gly Val Tyr Leu Arg Pro Ser Ser His Ser 130 135 140

Thr Asp Lys Asp Ser Leu Ala Ser Val Met Tyr Met Val Val Thr Pro 145 150 155 160

Met Leu

<210> 303

<211> 487

<212> DNA

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  Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg
                                        10
ctg tgt gga ctg ctg gtt ctg gca tcc tgg atc ctg agt gcc ctg aat
                                                                         97
Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
            20
tcc tca tta caa acc tta ata gtg ctg cgg ctt tcc ttc tgc aca gac
                                                                         145
Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp
ttg gaa atc ccc cac ttt ttc tgc gaa ctt aat cag gtc atc cac ctt
                                                                         193
Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu
    50
gcc tgt tct gac act ttt ctt aat gat gtg gtg atg tat ttg gcc gct
                                                                         241
Ala Cys Ser Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala
                                                                         289
gtg ctg ctg ggg ggt ggt ccc ctt gca ggg att ctt tac tct tac tct
Val Leu Leu Gly Gly Gly Pro Leu Ala Gly Ile Leu Tyr Ser Tyr Ser
                                                                         337
aag ata gtt tcc tcc ata cgt gca atc tca tca gct cag ggg aag tac
Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr
                                  105
             100
aag gca ttt tcc acc tgt gta tct cac atc tta att gtc tcc tta ttt
                                                                         385
Lys Ala Phe Ser Thr Cys Val Ser His Ile Leu Ile Val Ser Leu Phe
                              120
tat ggt aca ctc cta ggt gtg tac ctt agt tct gct gca act ggc aac
                                                                         433
Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn
                          135
    130
tca cat tca aga gct gca gcc tcg gtg atg tac act gtg gtc acc ccc
Ser His Ser Arg Ala Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro
                                                                         481
                                                                160
                                          155
                                                                         487
atg ctg
Met Leu
<210> 304
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Ala Cys Ser Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala 65 70 75 80

Val Leu Gly Gly Gly Pro Leu Ala Gly Ile Leu Tyr Ser Tyr Ser 85 90 95

Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr
100 105 110

Lys Ala Phe Ser Thr Cys Val Ser His Ile Leu Ile Val Ser Leu Phe 115 120 125

Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn 130 135 140

Ser His Ser Arg Ala Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro 145 150 155 160

Met Leu

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tct Ser	aca Thr	att Ile 35	cac His	acc Thr	agc Ser	tct Ser	atg Met 40	ttg Leu	aga Arg	ctc Leu	ttt Phe	ctg Leu 45	tgc Cys	aaa Lys	act Thr	145
aat Asn	gtg Val 50	att Ile	aac Asn	cat His	tat Tyr	ttt Phe 55	tgt Cys	gat Asp	ctc Leu	ttc Phe	.cct Pro 60	ctc Leu	ttg Leu	gaa Glu	ctc Leu	193
tcc Ser 65	tgc Cys	tcc Ser	agt Ser	acc Thr	tac Tyr 70	atc Ile	aat Asn	gaa Glu	tta Leu	cta Leu 75	gtt Val	ctg Leu	gtc Val	ttg Leu	agt Ser 80	241
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ttc Phe	acc Thr	att Ile	gcc Ala 100	Ser	atc Ile	ctc Leu	cac His	att Ile 105	ALG	tcc Ser	act Thr	gag Glu	ggc Gly 110	_	tcc Ser	337
aaa Lys	gcc Ala	ttc Phe 115	Ser	act Thr	tgc Cys	agc Ser	tcc Ser 120	1110	atc Ile	tca Ser	gct Ala	gtt Val 125		gtc Val	ttc Phe	385
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atg Met	Asp	caç Glr	n Gly 9 999	g aaa y Lys	gtg Val	. ser	tct Sei	gto Val	g ttt l Phe	tac Tyr 155		a act	gtt Val	gtq L Va	g ccc l Pro 160	481
_	g ctg Lei															487
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Ph	ie Cy	rs Ph	ne Ai 20	g Le	eu Th	ır Va	il G	Ly Va 25	al Ty	yr Il	e Le	eu Gi	ly I] 30	le Le )	eu Gly	
Se	er Th	nr II 35		is Th	ır Se	er Se	er Me	et Lo	eu A:	rg Le	eu Pl	ne L	eu Cy 5	ys L	ys Thr	

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Ser 65	Cys	Ser	Ser	Thr	Tyr 70	Ile	Asn	Glu	Leu	Leu 75	Val	Leu	Val	Leu	Ser 80		
Ala	Leu	Asn	Ile	Leu 85	Thr	Pro	Ala	Leu	Thr 90	Ile	Leu	Ala	Ser	Tyr 95	Ile		
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Lys	Ala	Phe 115	Ser	Thr	Cys	Ser	Ser 120	His	Ile	Ser	Ala	Val 125	Ala	Val	Phe		
Phe	Gly 130		Ala	Ala	Phe	Met 135	Tyr	Leu	Gln	Pro	Ser 140	Ser	Val	Ser	Ser		
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Met	Leu																
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tta Lei	a tgo ı Cys	tgt Cys	gte Val	g ttg L Lei	g gtt 1 Val	gct Ala	gco Ala	c tco a Sei 25	c tgg r Trp	g ato Met	g gga : Gly	a gga / Gly	ttt Phe 30	gto Val	g cac L His	9	97
tco Sei	aco Thi	gto Val	c caq l Gli	g aco	att Ile	cto Lei	act Thi 40	t ato	c cgt e Arg	t cto g Lei	g cco	ttt Phe 45	e Cy:	ggg Gl	g cca y Pro	14	15
aat Asi	c caq n Gli 50	g gte n Va	g ga l As	c aad p Asi	c ttt n Phe	ttt Phe 55	tg: Cy:	t ga s As	t gti p Vai	t cco	e cct Pro 60	t gto o Vai	c ate	c aaa e Ly	a ctt s Leu		93
gc	c tg	t gc	t ga	c ac	t tti	gto	c at	t ga	a tt	g cto	c at	g gta	a tc	t aa	c agt	24	41

65	Asp Thr	Phe Val	Ile G	lu Leu	Leu Met 75	Val Se	er Asn	Ser 80	
ggg ttg atc Gly Leu Ile	tcc acc Ser Thr 85	agc tcc Ser Ser	ttt g Phe V	gtg gtg Val Val 90	ctg att Leu Ile	tcc tc Ser Se	cc tac er Tyr 95	acc Thr	289
act atc cta Thr Ile Leu	gtc aag Val Lys 100	att cac	Ser I	aag gag Lys Glu 105	gga agg Gly Arg	cga aa Arg Ly 11	s Ala	ctc Leu	337
tcc aca tgt Ser Thr Cys 115	gcc tct Ala Ser	cac ctt His Leu	atg g Met V 120	gtg gta Val Val	aca ctt Thr Leu	ttt gg Phe Gl 125	ga ccc Ly Pro	tgt Cys	385
agt ttc atc Ser Phe Ile 130	tat cct Tyr Pro	cat cct His Pro	Phe S	tct aca Ser Thr	ttt tct Phe Ser 140	Val As	ac aag sp Lys	atg Met	433
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<pre>&lt;400&gt; 308  Val Ala Ile 1  Leu Cys Cys Ser Thr Val</pre>	e Cys Hi 5 s Val Le 20	s Pro Le u Val Al r Ile Le	u His da Ala u Thr 40 e Cys	Tyr Thr 10 " Ser Trp 25	Thr Val	Gly P 3 Phe C 45	er Arg 15 The Val 0	Gly His Pro	
<pre>&lt;400&gt; 308  Val Ala Ile 1  Leu Cys Cys  Ser Thr Va. 35  Asn Gln Va</pre>	e Cys Hi 5 s Val Le 20 l Gln Th	s Pro Le u Val Al r Ile Le n Phe Ph	u His a Ala u Thr 40 e Cys	Tyr Thr 10 Ser Trp 25 Ile Arg	Met Gly Leu Pro Pro Pro	Gly P 3 Phe C 45	er Arg 15 The Val 0 Cys Gly	Gly His Pro Leu	
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<pre>&lt;400&gt; 308  Val Ala Ile 1  Leu Cys Cys  Ser Thr Va. 35  Asn Gln Va 50  Ala Cys Al 65</pre>	e Cys Hi 5  Val Le 20  I Gln Th  I Asp As  A Asp Th  e Ser Th	s Pro Le u Val Al r Ile Le n Phe Ph 55 r Phe Va 70	u His a Ala u Thr 40 e Cys l Ile	Tyr Thr 10 " Ser Trp 25  Ile Arg Asp Val Glu Leu Val Val 90	Thr Value of Met Gly Leu Pro Pro 60 Leu Me 75 Leu Il	Met S  Gly P  3  Phe C  45  Val I  t Val S  e Ser S	er Arg 15 The Val 0 Tys Gly The Lys Ger Asn Ger Tyr 95	Gly His Pro Leu Ser 80	

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Ser Phe Ile Tyr Pro His Pro Phe Ser Thr Phe Ser Val Asp Lys Met

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- Ile Cys Val Thr Met Ile Ile Val Cys Trp Ser Ile Ser Ile Ala Gly
- Ala Leu Ile Leu Thr Val Phe Thr Met His Leu Pro Tyr Cys Gly Pro
- Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Leu Lys Leu
- Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Ile Leu Gly 70
- Phe Ile Leu Leu Val Pro Leu Ser Leu Ile Leu Ala Ser Tyr Val
- Phe Ile Phe Ala Ser Ile Phe Arg Ile Arg Ser Ala Gln Gly Arg Leu 105
- Lys Ser Phe Ser Thr Cys Ala Ser His Val Thr Val Val Thr Met Phe
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Phe Leu

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ctt tgt gtc cag cta gtg gct gga ctg tgg ctt gtt act tac ctc cat
                                                                           97
Leu Cys Val Gln Leu Val Ala Gly Leu Trp Leu Val Thr Tyr Leu His
                                  25
                                                                          145
gcc ctc ctg cat act tcc cta ata gca cat ctg tcc ttc tgt gcc ttc
Ala Leu Leu His Thr Ser Leu Ile Ala His Leu Ser Phe Cys Ala Phe
        3.5
                                                                          193
aat atc atc cat cat ttc ttc tgt gat ctc aac cct cta cta cgg ctc
Asn Ile Ile His His Phe Phe Cys Asp Leu Asn Pro Leu Leu Arg Leu
                          55
tot tgo tot goo gto too tto aac gta atg atc att ttt gca gta gga
                                                                          241
Ser Cys Ser Ala Val Ser Phe Asn Val Met Ile Ile Phe Ala Val Gly
                     70
ggt cta ttg gct ctc acg ccc ctt gtc tgt atc ctc gta ttt tat gga
                                                                          289
Gly Leu Leu Ala Leu Thr Pro Leu Val Cys Ile Leu Val Phe Tyr Gly
                                       90
                                                                          337
ctt atc ttc tcc act gtt ctg aag atc acc tct act cag ggg aaa cag
Leu Ile Phe Ser Thr Val Leu Lys Ile Thr Ser Thr Gln Gly Lys Gln
                                  105
             100
aga gct gct tcc acc tgc ggc tgc cac ctg tca gta gtg gtg ctg ttt
Arg Ala Ala Ser Thr Cys Gly Cys His Leu Ser Val Val Leu Phe
                                                                          385
tat ggc aca gcc att gcc gtc tac ttt agc ccc tca tcc tcc cat acg
                                                                          433
Tyr Gly Thr Ala Ile Ala Val Tyr Phe Ser Pro Ser Ser Ser His Thr
                          135
     130
cct gag agt gac act ctc tcg acc gtc atg tat tca gtg gtg gcc ccg
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 Pro Glu Ser Asp Thr Leu Ser Thr Val Met Tyr Ser Val Val Ala Pro
                                                                 160
                                           155
 145
                                                                           487
 atg ctg
Met Leu
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Ala	Leu	Leu 35	His	Thr	Ser	Leu	Ile 40	Ala	His	Leu	Ser	Phe 45	Cys	Ala	Phe
Asn	Ile 50	Ile	His	His	Phe	Phe 55	Cys	Asp	Leu	Asn	Pro 60	Leu	Leu	Arg	Leu
Ser 65	Cys	Ser	Ala	Val	Ser 70	Phe	Asn	Val	Met	Ile 75	Ile	Phe	Ala	Val	Gly 80
Gly	Leu	Leu	Ala	Leu 85	Thr	Pro	Leu	Val	Cys	Ile	Leu	Val	Phe	Tyr 95	Gly
Leu	Ile	Phe	Ser 100	Thr	Val	Leu	Lys	Ile 105	Thr	Ser	Thr	Gln	Gly 110	Lys	Gln
Arg	Ala	Ala 115		Thr	Cys	Gly	Cys 120	His	Leu	Ser	Val	Val 125	Val	Leu	Phe
Tyr	Gly 130		Ala	Ile	Ala	Val 135		Phe	Ser	Pro	Ser 140	Ser	Ser	His	Thr
Pro 145		Ser	Asp	Thr	Leu 150		Thr	Val	Met	Tyr 155	Ser	Val	Val	Ala	Prc 160
Met	Leu	ı													
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                                                                     300
cagcattete cacattaget cacagaggge aggteaggte taaageette agtaeetgea
                                                                     360
gttcccacat aattgtggta tcgcttttct ttgggtcagg tgctttcatg tacctcaaac
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tggccaggtt gtgtttttgt gcagacaatg tgatccccca ctttttctgt gatatgtctg
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ctctgctgaa gctgtcctgc tctgacactc gagttaatga attggtgata tttatcatgg
                                                                      240
gagggeteat tettgteate ceatteetae teateettgg gteetatgea egaattgtet
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cetecatect caaggteect tetaagggta tetgeaagge ettetetaet tgtggeteec
                                                                      360
acctctctgt ggtgtccctg ttctatggga ccgttagtgg tctctactta tgcccatcgg
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 cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt
                                                                        96
 Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
                                 25
 gct ctt ttg cat acc ctc ctt ctg gcc cgg ctt tcc ttc tgt gct gac
                                                                       144
 Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp
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tcc Ser 65	tgc Cys	tca Ser	gac Asp	acc Thr	tcc Ser 70	ctc Leu	aat Asn	cag Gln	tta Leu	gca Ala 75	atc Ile	ttt Phe	aca Thr	gca Ala	gga Gly 80		2	40
ttg Leu	aca Thr	gcc Ala	att Ile	atg Met 85	ctt Leu	cca Pro	ttc Phe	ctg Leu	tgc Cys 90	atc Ile	ctg Leu	gtt Val	tct Ser	tat Tyr 95	ggt Gly		2	88
cac His	att Ile	gly ggg	gtc Val 100	acc Thr	atc Ile	ctc Leu	cag Gln	att Ile 105	ccc Pro	tcc Ser	acc Thr	aag Lys	ggc Gly 110	ata Ile	tgc Cys		3	36
aaa Lys	gcc Ala	ttg Leu 115	tcc Ser	act Thr	tgt Cys	gga Gly	tcc Ser 120	cac His	ctc Leu	tca Ser	gtg Val	gtg Val 125	act Thr	atc Ile	tat Tyr		3	84
tat Tyr	999 Gly 130	aca Thr	att Ile	att Ile	ggt Gly	ctc Leu 135	tat Tyr	ttt Phe	cta Leu	ccc Pro	cca Pro 140	tcc Ser	agc Ser	aac Asn	acc Thr		4	32
aat Asn 145	gac Asp	aag Lys	aac Asn	ata Ile	att Ile 150	gct Ala	tca Ser	gtg Val	ata Ile	tac Tyr 155	aca Thr	gta Val	gtc Val	act Thr	ccc Pro 160		4	80
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Gln	Cys	: Val	Met 20	Leu	Val	Ala	Gly	Ser 25	Trp	Val	Ile	Ala	Cys	Ala	. Cys			
Ala	Leu	Leu 35	His	Thr	· Leu	Leu	Leu 40	Ala	Arg	Leu	Ser	Phe 45	Cys	Ala	Asp			
His	50 50 50 50 50 50 50 50 50 50 50 50 50 5	: Ile	Ser	His	Phe	Phe 55	. Cys	Asp	Leu	Gly	Ala 60	. Leu	. Leu	. Lys	. Leu			
Ser 65	Суя	s Ser	Asp	Thr	Ser 70	Leu	ı Asn	Glr	Lev	Ala 75	ılle	Phe	Thr	Ala	Gly 80			

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His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
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Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
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                                                                       120
 attttccttc tcctactgtg ggtctcggga aatagcccac ttcttctgtg agttcccttc
                                                                       180
 catactaatc ctctcatgca atgacacatc aatatttgaa aaggttcttt tcatctgctg
                                                                       240
 tatagtaatg attgtttttc ctgttgcaat catcatcgct tcctatgctc aagttattct
                                                                       300
 ggctgtcatt cacatgggat ctggagaggg tcgtcggata gctttcacga cctgttcctc
                                                                       360
 teaceteatg gtggtgggaa tgtactatgg ageagetttg tteatgtaca taeggeeeac
                                                                       420
 atctgatcgc tcccctacac aggacaagat ggtgtctgta ttctacacca tcctcactcc
                                                                       480
                                                                       487
 catgctg
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<223> Taxon = 9600; gene = PPY114; Accession DDBJ/EMBL/GenBank = AF179816

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 Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
ctc tgt ctc tcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat
                                                                          97
Leu Cys Leu Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
                                                                         145
gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
        3.5
aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg
                                                                         193
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
    50
tcc tgc tct gac act cga gtt aat gaa ttg gtg ata ttt atc atg gga
Ser Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
                                                                         241
                     70
ggg ctc att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca
                                                                         289
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
                                      90
                                                                         337
cga att gtc tcc tcc atc ctc aag gtc cct tct aag ggt atc tgc aag
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Lys Gly Ile Cys Lys
                                  105
            100
                                                                         385
ged the tet act tgt ggd ted cac etc tet gtg gtg ted etg the tat
Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr
                                                   125
                              120
        115
ggg acc gtt agt ggt ctc tac tta tgc cca tcg gct aat agt tct act
                                                                         433
Gly Thr Val Ser Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr
ctg aag gag act gtc atg gct gta atg tac act gtg gtg acc ccc atg
                                                                         481
Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Val Thr Pro Met
                                          155
                     150
145
                                                                         484
ctq
Leu
<210> 319
<211> 161
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            20
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
                            40
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
                                            60
Ser Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
                    70
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Lys Gly Ile Cys Lys
Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr
                             120
Gly Thr Val Ser Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr
Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Val Thr Pro Met
                    150
Leu
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                                                                        48
 Val Ala Val Cys His Pro Leu His Tyr Thr Leu Ile Met His Gly Gly
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96

144

tee etg atg gaa aca att ate ace tte eag ett ete etg tgt eae aat

2.0

Ser Leu Met Glu Thr 35	Ile Ile Thr P	he Gln Leu Leu	Leu Cys His .	Asn
gtt att aat cac ttt Val Ile Asn His Phe 50	gcc tgt gag a Ala Cys Glu T 55	cc tta gca gtg hr Leu Ala Val 60	cta cga cta Leu Arg Leu	gcc 192 Ala
tgt gtg gac gtc tcc Cys Val Asp Val Ser 65	ttc aac aag g Phe Asn Lys A 70	cc atg gtg gcc la Met Val Ala 75	Ile Ser Gly	ttt 240 Phe 80
ctg gtg atc ctg ctt Leu Val Ile Leu Leu 85	ccc tgt tca c Pro Cys Ser L	tg atc cta ttc eu Ile Leu Phe 90	tcc tat gct Ser Tyr Ala 95	cac 288 His
ata gtt gct gcc att Ile Val Ala Ala Ile 100	Leu His Ile P	ct tct gcc cag ro Ser Ala Gln 05	gga cgc cgc Gly Arg Arg 110	aaa 336 Lys
gcc ttt ggg act tgc Ala Phe Gly Thr Cys 115	acg tct cac c Thr Ser His L 120	tc act gtg gtt eu Thr Val Val	tgc atg tgc Cys Met Cys 125	ttt 384 Phe
ggg gct aca atg tto Gly Ala Thr Met Phe 130	acc tac atg a Thr Tyr Met A 135	ga cct gcg ggc rg Pro Ala Gly 140	Gly Ser Ser	ctg 432 Leu
gaa aag aag aat atg Glu Lys Lys Asn Met 145	gtt gcc ctc t Val Ala Leu F 150	tt tat gcc att The Tyr Ala Ile 155	gtg att cca Val Ile Pro	atg 480 Met 160
ctt Leu				483
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Leu Cys Leu Gly Le 20	u Val Ala Gly	Cys Leu Val Ala 25	a Gly Phe Met 30	Asn
Ser Leu Met Glu Th 35	r Ile Ile Thr 40	Phe Gln Leu Le	u Leu Cys His 45	Asn
Val Ile Asn His Ph 50	e Ala Cys Glu 55	Thr Leu Ala Va 60	l Leu Arg Leu	Ala
Cys Val Asp Val Se	_	nl- Mot Mal Al	a Tla Car Gly	, Phe

Leu va	l Ile		Leu 85	Pro	Cys	Ser :	Leu	Ile 90	Leu	Phe	Ser '	Tyr	Ala 95	His	
Ile Va	l Ala	Ala 100	Ile	Leu	His		Pro 105	Ser	Ala	Gln		Arg 110	Arg	Lys	
Ala Ph	e Gly 115	Thr	Cys	Thr		His 120	Leu	Thr	Val		Cys 125	Met	Cys	Phe	
Gly Al		Met	Phe		Tyr 135	Met	Arg	Pro	Ala	Gly 140	Gly	Ser	Ser	Leu	
Glu Ly 145	s Lys	Asn	Met	Val 150	Ala	Leu	Phe	Tyr	Ala 155	Ile	Val	Ile	Pro	Met 160	
Leu															
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								1	0	eu I			1	.5	•
ctg to Leu C	gc cto ys Lei	999 1 Gly 20	cta	gtg Val	gcc Ala	ggc Gly	tgc Cys 25	ctq	o gtg	gct	ggt	ttc	atg	, aat	97
Leu C	gc cto ys Leo tg ato eu Met 35	1 Gly 20	ctg Leu	Val att	Ala atc	acc	25 ttc	ctg Leu	gtg Val	gct Ala	ggt Gly ctg	tto Phe 30	atg Met	aat Asn	
tcc c Ser L gtt a Val I	ys Lei tg atg eu Mei	g gaa Glu	ctg Leu aca Thr	att Ile	atc Ile	acc Thr 40	ttc Phe	ctg Leu cag Gln	gtg Val ctt Leu	gct Ala ccc Pro	ggt Gly ctg Leu 45	ttc Phe 30 tgt Cys	atg Met cac His	aat Asn aat Asn	97
tcc c ser L gtt a Val I	ys Leu tg atg eu Met 35 tt aat le Ass	g gaa G Glu c cac	ctg Leu aca Thr	att Ile	atc Ile tgt Cys 55	acc Thr 40 gag Glu	ttc Phe acc	ctg Leu cag Gln tta	gtg Val ctt Leu gca Ala	gct Ala ccc Pro gtg Val 60	ggt Gly ctg Leu 45 cta Leu	tto Phe 30 tgt Cys	atg Met cac His cta	y aat Asn aat Asn agcc	97

ata Ile	gtt Val	gct Ala	gcc Ala 100	att Ile	ctt Leu	cgt Arg	Ile	cct Pro 105	tct Ser	gcc Ala	cag Gln	gga Gly	cac His 110	cgc Arg	aaa Lys	337
gcc Ala	ttt Phe	ggg Gly 115	acc Thr	tgc Cys	acg Thr	tct Ser	cac His 120	ctc Leu	act Thr	gtg Val	gtt Val	tgc Cys 125	atg Met	tgc Cys	ttt Phe	385
Gly aaa	gct Ala 130	aca Thr	atg Met	ttc Phe	acc Thr	tac Tyr 135	atg Met	aga Arg	cct Pro	gcg Ala	ggt Gly 140	ggc Gly	tcc Ser	tcc Ser	ctg Leu	433
gaa Glu 145	aag Lys	gag Glu	aat Asn	atg Met	gtt Val 150	gcc Ala	ctc Leu	ttt Phe	tat Tyr	gcc Ala 155	att Ile	gtg Val	att Ile	cca Pro	atg Met 160	481
ctt Leu																484
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1	Ala	vai	СуБ	5	FIO	БСС		-1-	10					15	-	
Leu	Cys	Leu	Gly 20	Leu	Val	Ala	Gly	Cys 25	Leu	Val	Ala	Gly	Phe 30	Met	Asn	
Ser	Leu	Met 35	Glu	Thr	Ile	Ile	Thr 40	Phe	Gln	Leu	Pro	Leu 45	Cys	His	Asn	
Val	Ile 50	Asn	His			Cys 55						Leu	Arg	Leu	Ala	
C	Val	Asp	Val	Ser		Asn	Lys	Ala	Thr	Val 75	Ala	Ile	Ser	Gly	Phe 80	,
65					70											
65		Ile	. Leu	Leu 85		Cys	Ser	Leu	Ile 90	Leu	Phe	Ser	Tyr	Ala 95	His	
65 Leu	. Val			85 Ile	Pro				90 Ser					95 Arg	His Lys	

Gly Ala Thr Met Phe Thr Tyr Met Arg Pro Ala Gly Gly Ser Ser Leu

130 135 140

Glu Lys Glu Asn Met Val Ala Leu Phe Tyr Ala Ile Val Ile Pro Met 145 150 155 160

Leu

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      324
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      DNA
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= AF179819
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                                                                      120
tgtgaacctg ccttttttgt ggacctaatg tagtagacag ctttttttgt gatcttcctc
                                                                      180
gagtgaccaa acttgcctgc ctggactctt acctcattga aatactaatt gtggtcaata
                                                                      240
gtggagttct ttccctaagc actttctgtc tcttggtcag ctcctacatc attattcttg
                                                                      300
                                                                      360
ttatggtttg gctcaagtct tcggctgcaa tggcgaaggc attttctacg ctggcttccc
atattgcagt agtaatatta ttctttggac cttgcatctt catctatgtg tggcccttta
                                                                      420
ccatctatcc tttggataaa cttcttgcca tattttacac tgttttcacc cccatccta
                                                                      479
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<223> Product = olfactory receptor
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                                                                       49
  Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt
                                                                       97
Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
                                 25
get ett ttg cat acc etc ett etg gee egg ett tee tte tgt get gae
                                                                       145
```

Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp

40 45 35 cac atc atc tct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ctg 193 His Ile Ile Ser His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 55 241 tcc tgc tca gac acc tcc ctc aat cag tta gca atc ttt aca gca gga Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 75 ttg aca gcc att atg ctt cca ttc ctg tgc atc ctg gtt tct tat ggt 289 Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 85 cac att ggg gtc acc atc ctc cag att ccc tcc acc aag ggc ata tgc 337 His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys 105 100 aaa gcc ttg tcc act tgt gga tcc cac ctc tca gtg gtg act atc tat Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 385 125 120 tat ggg aca att att ggt ctc tat ttt ctt ccc cca tcc agc aac acc 433 Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc 481 Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 155 150 487 atg ttg Met Leu <210> 326 <211> 162 <212> PRT <213> Pongo pygmaeus <220> <221> misc feature (1)..(487) <222> Taxon = 9600; gene = PPY118; Accession DDBJ/EMBL/GenBank = AF179820 <400> 326

Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys 20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp
35 40 45

His Ile Ile Ser His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 50 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 70 75 80

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Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
            100
                                105
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
                        135
    130
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
                    150
Met Leu
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       327
      475
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       DNA
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= AF179821
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ccagtggtag gctcttgggt cattggggtt atgcactccc tgagccagtt agctttcact
                                                                      120
gtaagettge cettetgtgg cecaaacata gtggacagtt attattgega cettaetttg
                                                                      180
gtcatcaaac gtgcctgtac agatgcttat atccctgaag tgttgatgct tttggacggt
                                                                      240
                                                                      300
ggtcttatgg gggtgaccat ttttgctttt gctgatctcc tacacggtca ttctgattac
tgtgcagcga cattectcag caggtatgge caaggeteae ageaetetga etgeecaeat
                                                                      360
tgctgtggtg accgtgttct ttgggccctg tatcttcatc tatgcctggc ctttcagcaa
                                                                      420
                                                                      475
cttaccagtg gataacattt tgtctgtatt ctctgtagtt ttcacaccta tatta
<210> 328
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       487
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       DNA
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       Pongo pygmaeus
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                                                                            49
    Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Thr Met Ser Gln Ser
                                          10
  cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt
                                                                            97
  Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
  gct ctt ttg cat acc ctc ctt ctg gcc cgg ctt tcc ttc tgt gct gac
                                                                           145
  Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp
  cac atc atc cct cac ttc ttc tgc gac ctt ggt gcc ctg ctc aag ctg
                                                                           193
  His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
                           55
  tcc tgc tca gac acc tcc ctc aat cag tta gca atc ttt aca gca gga
                                                                           241
  Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
  ttg aca gcc att atg ctt cca ttc ctg tgc atc ctg gtt tct tat ggt
                                                                           289
  Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
                                        90
                                                                           337
  cac att ggg gtc acc atc ctc cag att ccc tcc acc aag ggc ata tgc
  His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
                                    105
               100
  aaa gcc ttg tcc act tgt gga tcc cac ctc tca gtg gtg act atc tat
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
                                                                           385
                                120
  tat ggg aca att att ggt ctc tat ttt ctt ccc cca tcc agc aac acc
                                                                            433
  Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
       130
  aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc
                                                                            481
  Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
                                             155
                                                                            487
   atg ttg
  Met Leu
   <210> 329
   <211> 162
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          Pongo pygmaeus
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   <400> 329
   Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Thr Met Ser Gln Ser
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Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly

His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys 100

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 120

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr 135

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 155

Met Leu

<210> 330

<211> 487

<212> DNA <213> Saimiri sciureus

<220>

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<222> (1)..(487)

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<220>

<221> CDS

<222> (2)..(487)

Product = olfactory receptor

<400> 330

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ctc tgt gcc ttc tta gtg gct gta tct tgg att cca tct tgt gct agc 97 Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser 20

tcc ctc tct cac acc ctt ctg ctg acc ccg ctg cct ttc tgt gat gca 145 Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Pro Phe Cys Asp Ala 40 35

Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60	193
tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80	241
gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95	289
tac act ggg gcc act atc ctg agg gtc cct tca acc aaa ggg atc cgc Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg 100 105 110	337
aaa gcg ttg tcc atg tgt ggc tcc cgt ctc tct gtg gtg tct ctg tat Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr 115 120 125	385
tat ggc tca ata ttt ggc cag tac ctt ttc cca act gta agc agt tcc Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 130 135	433
att gac aag gat gtc att gtg gct cta atg tac aca gtg gtc aca ccc Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro 145 150 150	481
atg ctg Met Leu	487
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Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95														
Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg 100 105 110														
Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr 115 120 125														
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 130 135 140														
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro 145 150 155 160														
Met Leu														
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<220> <221> CDS <222> (2)(487)														
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<pre>&lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (2)(487) &lt;223&gt; Product = olfactory receptor  &lt;400&gt; 332 t gtt gcc ata tgt tac cct ctc cac tac act gcc atc atg agg gaa ggg    Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly    1</pre>														
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aaa gcg ttg tcc atg tgt ggc tcc cgt ctc tct gtg gtg tct ctg tat 385 Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr tat ggc tca ata ttt ggc cag tac ctt ttc cca act gta agc agt tcc 433 Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 135 att gac aag gat gtc att gtg gct cta atg tac aca gtg gtc aca ccc Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro 481 150 488 atg ctg t Met Leu

<210> 333

<211> 162 <212> PRT <213> Saimiri sciureus

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<400> 333

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Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser 25 2.0

Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala 35

Asn Thr Val His His Tyr Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 90

Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg 105 100

Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser 135 130

Ile	Asp	Lys	Asp	Val	Ile	Val	Ala	Leu	Met	Tyr	Thr	Val	Val	Thr	Pro
145					150					155					160

Met Leu

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<210>
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       Saimiri sciureus
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                                                                              49
  Val Ala Thr Cys His Pro Leu Arg Tyr Met Val Ile Met Asn Pro Cys
                                                                              97
ctc tgc agc ctg ctg att ctt ctt tct ccg ttg act agc gtt gtg aat
Leu Cys Ser Leu Leu Ile Leu Leu Ser Pro Leu Thr Ser Val Val Asn
gcc ctt ctt ctc agc ctg atg gtg ttg agg ctg tcc ttc tgc aca gat
Ala Leu Leu Ser Leu Met Val Leu Arg Leu Ser Phe Cys Thr Asp
                                                                             145
ctg gaa atc ccg ctc ttc ttc tgt gaa ctg gct cag gtc atc cag ctt
                                                                             193
Leu Glu Ile Pro Leu Phe Phe Cys Glu Leu Ala Gln Val Ile Gln Leu
                          55
gct tgt tct gac acc ctc atc aat aac atc ctg ata tat ttt gca gct
                                                                             241
Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ala
                      70
tgc ata ttt ggt ggt gtt cct ctg tct gga atc ata ttc tct tat gct
                                                                             289
Cys Ile Phe Gly Gly Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ala
                                        90
                                                                             337
cag att gcc tcc tct att ttg aga atg cca tca gca cgc aga aag tat
Gln Ile Ala Ser Ser Ile Leu Arg Met Pro Ser Ala Arg Arg Lys Tyr
                                                                             385
aaa gcc ttt tcc acc tgt ggg tct cac ctc tcc atg gtg ctc ttg ttc
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Met Val Leu Leu Phe
                               120
tat agg aca ggt ttg ggg gtg tac att agt tet gca gtt act gac tca
                                                                             433
Tyr Arg Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Thr Asp Ser
cct agg aag act gca gtg gct tca atg atg tat tct gtg ggt cct caa
Pro Arg Lys Thr Ala Val Ala Ser Met Met Tyr Ser Val Gly Pro Gln
                                                                             481
                                            155
145
                                                                             487
atg gtg
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<223> Taxon = 9521; gene = SSC186; Accession DDBJ/EMBL/GenBank = AF179825

<400> 335

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Leu Cys Ser Leu Leu Ile Leu Leu Ser Pro Leu Thr Ser Val Val Asn 20

Ala Leu Leu Ser Leu Met Val Leu Arg Leu Ser Phe Cys Thr Asp 35

Leu Glu Ile Pro Leu Phe Phe Cys Glu Leu Ala Gln Val Ile Gln Leu 55 50

Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ala

Cys Ile Phe Gly Gly Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ala 90

Gln Ile Ala Ser Ser Ile Leu Arg Met Pro Ser Ala Arg Arg Lys Tyr 110 105

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Met Val Leu Leu Phe 120 115

Tyr Arg Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Thr Asp Ser 130

Pro Arg Lys Thr Ala Val Ala Ser Met Met Tyr Ser Val Gly Pro Gln 160 145

Met Val

<210> 336 <211> 487 <212> DNA

<213> Saimiri sciureus

<220>

<400> 337

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<223> Taxon = 9521; gene = SSC187; Accession DDBJ/EMBL/GenBank = AF179826
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                                                                             49
c gtg gcc atc tgc ctc ccc cta cat tac gcc acc atc atg agc ccc atg
  Val Ala Ile Cys Leu Pro Leu His Tyr Ala Thr Ile Met Ser Pro Met
ctg tct cgc tcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat
Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
                                                                             97
             20
                                                                            145
gee atg ttg cae act tta ete atg gee agg ttg egt ttt tgt gea gae
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Arg Phe Cys Ala Asp
aat gtg atc ctc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg
                                                                            193
Asn Val Ile Leu His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
                          55
gcc tgc tct gac act cga gtt aat gaa ttg gtg ata ttt atc atg gga
                                                                            241
Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
                                            75
                                                                            289
ggc ctc att ctt gtc atc cca ttt cta ctt atc att ggg tcc tac gca
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala
cga att gtc ttc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc
                                                                            337
Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
                                   105
aag gcc gtc tct act tgt ggc tcc cac ctc tct gtg gtg tca ctg ttc
                                                                            385
Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
tat ggg act gtt att ggt ctc tac tta tgc cca tca gct aat aat tct
                                                                            433
Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser
act cta aag gag act gtc atg gct gtg atg tac act gtg atg gcc ccc
Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro
                                                                             481
                                            155
                      150
                                                                             487
 atg ctg
Met Leu
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        162
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Val Ala Ile Cys Leu Pro Leu His Tyr Ala Thr Ile Met Ser Pro Met 1 10 15

Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
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Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Arg Phe Cys Ala Asp

Asn Val Ile Leu His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu

Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly 65 70 75 80

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala 85 90 95

Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys 100 105 110

Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 115 120 125

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser 130 135 140

Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro 145 150 155 160

Met Leu

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<210> 338
<211> 487
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<222>
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                                                                       49
  Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Met Ser Ser Lys
atc tgc ctg cag ctt gtg ctt ggg tgc tgg gtt ctt ggt ttt ctc atc
                                                                      97
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Ile	Сув	Leu	Gln 20	Leu	Val	Leu	Gly	Cys 25	Trp	Val	Leu	Gly	Phe 30	Leu	Ile		
atc Ile	ttt Phe	cca Pro 35	cca Pro	ctc Leu	ctc Leu	tta Leu	gga Gly 40	cta Leu	aat Asn	ctt Leu	gac Asp	ttc Phe 45	tgt Cys	gcc Ala	tcc Ser		145
aac Asn	gtc Val 50	gtt Val	gat Asp	cat His	ttc Phe	tac Tyr 55	ttt Phe	gac Asp	act Thr	atc Ile	ccg Pro 60	ctc Leu	ctg Leu	cag Gln	att Ile		193
tcc Ser 65	tgc Cys	aca Thr	gac Asp	acg Thr	cag Gln 70	ctc Leu	ctg Leu	gag Glu	agg Arg	atg Met 75	gga Gly	ttc Phe	atc Ile	tca Ser	gcg Ala 80		241
ttg Leu	gtg Val	aca Thr	ctc Leu	tta Leu 85	gtc Val	aca Thr	ttg Leu	gta Val	atg Met 90	gtg Val	ata Ile	ata Ile	tca Ser	tat Tyr 95	act Thr		289
tat Tyr	att Ile	gcc Ala	ctg Leu 100	aca Thr	att Ile	cta Leu	aaa Lys	atc Ile 105	cct Pro	tca Ser	act Thr	agt Ser	cag Gln 110	agg Arg	aaa Lys		337
aag Lys	gct Ala	ttt Phe 115	tcc Ser	acg Thr	tgt Cys	tct Ser	tct Ser 120	cac His	atg Met	att Ile	gtg Val	ata Ile 125	tcc Ser	ctt Leu	tct Ser		385
tat Tyr	ggc Gly 130	Ser	tgc Cys	atc Ile	ttc Phe	atg Met 135	tat Tyr	gtt Val	aag Lys	cca Pro	tca Ser 140	vaı	aaa Lys	caa Gln	agg Arg		433
gta Val 145	Ser	ttt Phe	tca Ser	aag Lys	gga Gly 150	Ile	tcg Ser	gtg Val	ctc Leu	aat Asn 155	Thr	tct Ser	gtt Val	gct Ala	cca Pro 160		481
	ttg Leu																487
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<22 <22 <22 <22	:1> :2>	(1)	c_fea (48 on =	71		ene =	= SSC	C190;	: Acc	cessi	lon I	DBJ,	/EMBI	L/Ger	nBank	= AF	7179827
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Val	Ala	a Ile	е Суя	5 Lys	s Pro	) Let	ı His	з Туз	Thi	r Thi	r Ile	e Met	: Sei	r Sei 15	. Lys		
Ile	e Cys	s Lei	u Gli 20	n Lei	ı Val	l Leı	ı Gl	y Cys 25	s Trj	p Val	l Le	u Gl	y Phe 30	e Lei	ıIle		
Ile	e Phe	e Pro	o Pr	o Le	u Le	u Lei	u Gl:	y Le	u Ası	n Lei	u As	p Pho 45	е Су	s Ala	a Ser		
As	n Va 50		l As	р Ні	s Ph	е Ту 55	r Ph	e As	p Th	r Il	e Pr 60	o Le	u Le	u Gl	n Ile		

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Ser Cys Thr Asp Thr Gln Leu Leu Glu Arg Met Gly Phe Ile Ser Ala
                     70
                                          75
Leu Val Thr Leu Leu Val Thr Leu Val Met Val Ile Ile Ser Tyr Thr
                85
Tyr Ile Ala Leu Thr Ile Leu Lys Ile Pro Ser Thr Ser Gln Arg Lys
            100
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser
                             120
Tyr Gly Ser Cys Ile Phe Met Tyr Val Lys Pro Ser Val Lys Gln Arg
Val Ser Phe Ser Lys Gly Ile Ser Val Leu Asn Thr Ser Val Ala Pro
                                          155
                     150
Leu Leu
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                                                                           48
Val Ala Ile Cys His Pro Leu Gln Tyr Ser Val Ile Met Thr Thr Gly
 tac tgt gga cag ctg gtg gct ttc tct tac atg agt ggt ttc atg atc
                                                                           96
Tyr Cys Gly Gln Leu Val Ala Phe Ser Tyr Met Ser Gly Phe Met Ile
             20
 tct gtc atc aag gtc tat ttc att tca cat gtt gct ttc tgt ggc tcc
Ser Val Ile Lys Val Tyr Phe Ile Ser His Val Ala Phe Cys Gly Ser
                                                                          144
                               40
                                                                          192
 aat gtt atg aac cac ttt ttc tgt gat atc tca cca gtc cta aaa ctg
 Asn Val Met Asn His Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu
 gca tgc aaa gac atg tcc aca gct gag cta gtg gac ttt gct tta gct
                                                                          240
 Ala Cys Lys Asp Met Ser Thr Ala Glu Leu Val Asp Phe Ala Leu Ala
                                           75
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atc gtc att ctt gtg atc cct ctc att acc act atc ctc tcc tat atc 288  Ile Val Ile Leu Val Ile Pro Leu Ile Thr Thr Ile Leu Ser Tyr Ile  85 90 95	
tac att gtc tcc gcc att ctg cat ata ccc tcc acc cag gga agg aag Tyr Ile Val Ser Ala Ile Leu His Ile Pro Ser Thr Gln Gly Arg Lys 100 105 110	
aag gcc ttc tcc acc tgt gca tct cac ctc act gta gtc ata att ttt Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe 115 120 125	
tac aca gcc atg att ttt aca tat gtt cgg ccc aga gct att gca tca  Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser  130  135  140	
ttt aat tcc aac aaa cta atg tca gct gtg tat gca gtc ctc aca ccc Phe Asn Ser Asn Lys Leu Met Ser Ala Val Tyr Ala Val Leu Thr Pro 145 150 155 160	
atg ct Met	
<210> 341 <211> 161 <212> PRT <213> Saimiri sciureus	
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<pre>&lt;222&gt; (1)(485) &lt;223&gt; Taxon = 9521; gene = SSC191; Accession DDBJ/EMBL/GenBank = AF1798 &lt;400&gt; 341</pre>	328
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<pre> &lt;222&gt; (1)(485) &lt;223&gt; Taxon = 9521; gene = SSC191; Accession DDBJ/EMBL/GenBank = AF1798  &lt;400&gt; 341  Val Ala Ile Cys His Pro Leu Gln Tyr Ser Val Ile Met Thr Thr Gly 1</pre>	328
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115 120 125

Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser . 130 135 140

Phe Asn Ser Asn Lys Leu Met Ser Ala Val Tyr Ala Val Leu Thr Pro 145 150 155 160

Met

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<210> 342
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                                                                          49
  Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
                                        10
                                                                          97
ctc tgt gcc ttc tta gtg gct gta tct tgg att cca tct tgt gct agc
Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
                                  25
                                                                         145
tcc ctc tct cac acc ctt ctg ctg acc ccg ctg tct ttc tgt gat gca
Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala
                                                   45
aac acc gtc cac cac ttc ttc tgt gac ctt gct gcc ctg ctc aag ctg
                                                                         193
Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
                         55
tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg
                                                                         241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc
                                                                         289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
                                      90
tac act ggg gcc act atc ctg agg gtc cct tca acc aaa ggg atc cgc
Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
                                                                          337
             100
aaa gcg ttg tcc atg tgt ggc tcc cgt ctc tct gtg gtg tct ctg tat
                                                                          385
Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
                              120
         115
tat ggc tca ata ttt ggc cag tac ctt ttc cca act gta agc agt tcc
                                                                          433
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
                          135
     130
```

Met Leu

att gac aag Ile Asp Lys 145	gat gtc Asp Val	att gtg go Ile Val Al 150	ct cta a la Leu M	atg tac Met Tyr 155	aca gtg Thr Val	gtc aca Val Thr	ccc 481 Pro 160
atg ctg Met Leu							487
<210> 343 <211> 162 <212> PRT <213> Sain	niri sciur	reus					
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Leu Cys Al	a Phe Leu 20	Val Ala V	al Ser 25	Trp Ile	Pro Ser	Cys Ala 30	Ser
Ser Leu Se 35	r His Thr	Leu Leu L		Pro Leu	Ser Phe 45	Cys Asp	Ala
Asn Thr Va 50	l His His	Phe Phe C	ys Asp	Leu Ala	Ala Leu 60	Leu Lys	Leu
Ser Cys Se 65	r Asp Ile	Phe Leu A	sn Glu	Leu Val 75	Met Phe	Thr Val	Gly 80
Val Val Va	l Ile Thr 85	Leu Pro F	he Met	Cys Ile 90	Leu Val	Ser Tyr 95	Gly
Tyr Thr Gl	y Ala Thr 100	Ile Leu A	arg Val 105	Pro Ser	Thr Lys	Gly Ile 110	Arg
Lys Ala Le			Ser Arg	Leu Ser	Val Val 125	Ser Leu	Tyr
Tyr Gly Se	r Ile Phe	Gly Gln 7	Yr Leu	Phe Pro	Thr Val	Ser Ser	Ser
Ile Asp Ly 145	s Asp Val	Ile Val A	Ala Leu	Met Tyr 155	Thr Val	Val Thr	Pro 160

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                                                                        49
 Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
ctc tgt gcc ttc tta gtg gct gta tct tgg att cca tct tgt gct agc
                                                                        97
Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
tee etc tet cae ace ett etg etg ace eeg etg tet tte tgt gat gea
                                                                       145
Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala
                                                                       193
aac acc gtc cac cac ttc ttc tgt gac ctt gct gcc ctg ctc aag ctg
Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
                        55
                                                                       241
tee tge tea gat ate tte ete aat gag etg gte atg tte aca gta ggg
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
                     70
gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc
                                                                       289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
tac act ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cgc
                                                                       337
Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
                                 105
aaa gcg ttg tcc atg tgt ggc tcc cgt ctc tct gtg gtg tct ctg tat
                                                                       385
Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
                                                  125
                             120
tat ggc tca ata ttt ggc cag tac ctt ttc cca act gta agc agt tcc
                                                                        433
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
                                                                        481
att gac aag gat gtc att gtg gct cta acg tac aca gtg gtc aca ccc
Ile Asp Lys Asp Val Ile Val Ala Leu Thr Tyr Thr Val Val Thr Pro
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                     150
145
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 atg ctg
Met Leu
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<sup>&</sup>lt;213> Saimiri sciureus

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Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala
         35
Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
     50
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
                     70
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
                                      90
 Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
                                                      110
 Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
                              120
 Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
 Ile Asp Lys Asp Val Ile Val Ala Leu Thr Tyr Thr Val Val Thr Pro
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 Met Leu
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 <222> (2)..(484)
 <223> Product = olfactory receptor
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ctg tgt gga ct Leu Cys Gly Le 20	eu Leu Val	ctg gca tco Leu Ala Ser 25	c tgg atc ct c Trp Ile Le	g agt gcc ctg u Ser Ala Leu 30	aat 97 Asn
tcc tca tta ca Ser Ser Leu Gl 35	aa acc tta ln Thr Leu	ata gtg ctg Ile Val Lev 40	g cgg ctt tc ı Arg Leu Se	c ttc tgc aca r Phe Cys Thr 45	gac 145 Asp
ttg gaa atc co Leu Glu Ile Pi 50	cc cac ttt ro His Phe	ttc tgc gaa Phe Cys Glu 55	a ctt aat ca u Leu Asn Gl 60	n Val Ile His	ctt 193 Leu
gcc tgt tat ga Ala Cys Tyr As 65	ac act ttc sp Thr Phe 70	ctt aat gat Leu Asn As	t gtg gtg at p Val Val Me 75	g tat ttg gca t Tyr Leu Ala	gct 241 Ala 80
atg ctg ctg g Met Leu Leu G	gc ggt ggt ly Gly Gly 85	ccc ctc acc Pro Leu Th	a gga att at r Gly Ile Il 90	t tac tct tac e Tyr Ser Tyr 95	tct 289 Ser
Lys Ile Val S	cc tcc ata Ser Ser Ile	cgt gca at Arg Ala Il	e Ser Ser Al	ct cag ggg aag a Gln Gly Lys 110	tac 337 Tyr
aag gcg ttt t Lys Ala Phe S 115	cc acc tgt Ger Thr Cys	gca tct ca Ala Ser Hi 120	c atc tta at s Ile Leu Il	t gtc tcc tta Le Val Ser Leu 125	ttt 385 Phe
tat ggt aca c Tyr Gly Thr L 130	ctc cta ggt Leu Leu Gly	gtg tac at Val Tyr Il 135	e Ser Ser Al	ct gca act ggc la Ala Thr Gly 10	aac 433 Asn
tca cat tca a Ser His Ser S 145	agt gct gca Ser Ala Ala 150	gcc ttg gt Ala Leu Va	g atg tac ac 1 Met Tyr Th 155	ct gtg gtc acc hr Val Val Thr	ccc 481 Pro 160
atg ct Met					486
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	Leu Leu Val 20	Leu Ala Se 2!	er Trp Ile L 5	eu Ser Ala Le 30	u Asn





Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp 35 40

Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu 55

Ala Cys Tyr Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala

Met Leu Leu Gly Gly Gly Pro Leu Thr Gly Ile Ile Tyr Ser Tyr Ser

Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr 105

Lys Ala Phe Ser Thr Cys Ala Ser His Ile Leu Ile Val Ser Leu Phe 120 115

Tyr Gly Thr Leu Leu Gly Val Tyr Ile Ser Ser Ala Ala Thr Gly Asn 130 135

Ser His Ser Ser Ala Ala Ala Leu Val Met Tyr Thr Val Val Thr Pro 155 150

Met

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<211> 487

<212> DNA

<213> Saimiri sciureus

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(2)..(487) <222>

<223> Product = olfactory receptor

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gct gtg gct cat atg gga aac ata atg ttt atg acc ttt tgt tca gaa 145 Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu 45

aat ctt gtc aat cac tac atg tgt gat gtc ctt ccc ctc ctt gag ctc 193 Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Glu Leu

55 tcc tgc aac agc tct tac ata aat ttg ctg ttg gtt ttt att att gtg 241 Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val gcc att ggc att ggg gtg cca att gtc acc att ttt atc tct tat ggt 289 Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly 90 85 ttt att ctt tcc agc att ctc cac att agc tcc aca gag ggc agg tct 337 Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser 105 385 aaa gcc ttc agt acc tgc agc tcc cac ata att gtg gta tcg ctt ttc Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe 115 ttt ggg tca gga gct ttt atg tac ctc aaa cca cct tct att cta ccc Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro 433 135 130 ctg gac cag ggg aaa gtg tct tcc att ttt tat act gca gtg gtg ccc 481 Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro 155 150 487 atg ttt Met Phe <210> 349 <211> 162 <212> PRT <213> Saimiri sciureus <220> <221> misc\_feature (1)..(487) <222> Taxon = 9521; gene = SSC195; Accession DDBJ/EMBL/GenBank = AF179832 <223> <400> 349 Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu 35 Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu

50 55 60

Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val 65 70 75 80

Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly 85 90 95

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Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser
                                105
            100
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe
Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
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Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro
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Met Phe
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= AF179833
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                                                                      120
cetecatatt cectactgea ggtetagage cattgaceat ttettetgeg acateceage
                                                                      240
catgttgctt ctcgcctgta cggacacttg ggtctatgaa tacatggttt ttctaagtac
aagetgeett eteetette ttteettgge ateacegett eetatggeeg agteetattt
                                                                      300
gctgtctacc atacgcattc aaaaaaggga agaaaaaagg cctccaccac catttcaacc
                                                                      360
catttaactg tagtgatctt ttactatgca ccttttgtct acacctatct tcggcccagg
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aatctccact caccatccga agacaagatc ctggcagtct tctacaccat ccttacccct
                                                                      480
                                                                       486
atgctc
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 <223> Product = olfactory receptor
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atc tgc ctg cag ctt gtg ctt ggg tgc tgg gtt ctt ggt ttt ctc atc Ile Cys Leu Gln Leu Val Leu Gly Cys Trp Val Leu Gly Phe Leu Ile 20 25 30	97
atc ttt cca cca ctc ctc tta gga cta aat ctt gac ttc tgt gcc tcc Ile Phe Pro Pro Leu Leu Leu Gly Leu Asn Leu Asp Phe Cys Ala Ser 35 40 45	145
aac gtc gtt gat cat ttc tac tgt gac act atc ccg ctc ctg cag att Asn Val Val Asp His Phe Tyr Cys Asp Thr Ile Pro Leu Leu Gln Ile 50 55 60	193
tcc tgc aca gac acg cag ctc ctg gag agg atg gga ttc atc tca gcg Ser Cys Thr Asp Thr Gln Leu Leu Glu Arg Met Gly Phe Ile Ser Ala 65 70 75 80	241
ctg gtg aca ctc tta gtc aca ttg gta atg gtg ata ata tca tat act Leu Val Thr Leu Val Thr Leu Val Met Val Ile Ile Ser Tyr Thr 85 90 95	289
tat att gcc ctg aca att cta aaa atc cct tca act agt cag agg aaa Tyr Ile Ala Leu Thr Ile Leu Lys Ile Pro Ser Thr Ser Gln Arg Lys 100 105 110	337
aag gct ttt tcc acg tgt tct tct cac atg att gtg ata tcc ctt tct Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser 115 120 125	385
tat ggc agc tgc atc ttc atg tat gtt aag cca tca gtc aaa caa agg Tyr Gly Ser Cys Ile Phe Met Tyr Val Lys Pro Ser Val Lys Gln Arg 130 135 140	433
gta tct ttt tca aag gga att tcg gtg ctc aat acc tct gtt gct cca Val Ser Phe Ser Lys Gly Ile Ser Val Leu Asn Thr Ser Val Ala Pro 145 150 155 160	481
ctt ttg Leu Leu	487
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Ile Cys Leu Gln Leu Val Leu Gly Cys Trp Val Leu Gly Phe Leu Ile 20 25 30	

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Ile Phe Pro Pro Leu Leu Gly Leu Asn Leu Asp Phe Cys Ala Ser
Asn Val Val Asp His Phe Tyr Cys Asp Thr Ile Pro Leu Gln Ile
                        55
Ser Cys Thr Asp Thr Gln Leu Leu Glu Arg Met Gly Phe Ile Ser Ala
Leu Val Thr Leu Leu Val Thr Leu Val Met Val Ile Ile Ser Tyr Thr
                                                        95
Tyr Ile Ala Leu Thr Ile Leu Lys Ile Pro Ser Thr Ser Gln Arg Lys
                                105
            100
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser
Tyr Gly Ser Cys Ile Phe Met Tyr Val Lys Pro Ser Val Lys Gln Arg
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Val Ser Phe Ser Lys Gly Ile Ser Val Leu Asn Thr Ser Val Ala Pro
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Leu Leu
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                                                                      49
  Val Ala Ile Cys Phe Pro Leu His Tyr Thr Leu Leu Met Ser His Ser
att tgt gtc aac acg gtc att gtc tgt tgg tcc att agc ata gct ggg
                                                                      97
Ile Cys Val Asn Thr Val Ile Val Cys Trp Ser Ile Ser Ile Ala Gly
            20
gcc ctg atc tac act gtc ttc acc ttg cat ctg cct tat tgt ggc ccc
                                                                      145
Ala Leu Ile Tyr Thr Val Phe Thr Leu His Leu Pro Tyr Cys Gly Pro
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40

tac aag ata aac cac ttc ttc tgt gag gtc cct gct gtc ctg aag ttg

50 55 60	
gcc tgt gca gac aca tct ttt aat gac agg ctg gac ttc att ttg ggt Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Ile Leu Gly 65 70 75 80	241
ttc ctc ctg ctt ttg gtc cca ctc tcc ttc atc ctg gcc tct tac gta Phe Leu Leu Leu Val Pro Leu Ser Phe Ile Leu Ala Ser Tyr Val 85 90 95	289
ctc atc ttt gcc tct atc ttc aga atc cgc tca gtg cag ggg agg ctc Leu Ile Phe Ala Ser Ile Phe Arg Ile Arg Ser Val Gln Gly Arg Leu 100 105 110	337
aag too tto too acg tgt gct too cac gtc act gtg gtc acc atg ttc Lys Ser Phe Ser Thr Cys Ala Ser His Val Thr Val Val Thr Met Phe 115 120 125	385
tac gga ccg gcc atc atc atg tac atg agg ccc ggt tct tgg tat gac Tyr Gly Pro Ala Ile Ile Met Tyr Met Arg Pro Gly Ser Trp Tyr Asp 130 135 140	433
cca gag tgg gac aag aag gta gag gtg ttg tac aat gtc atc tct gcc Pro Glu Trp Asp Lys Lys Val Glu Val Leu Tyr Asn Val Ile Ser Ala 145 150 155 160	481
ttc ttg Phe Leu	487
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Leu	Ile	Phe	Ala 100	Ser	Ile	Phe	Arg	Ile 105	Arg	Ser	Val	Gln	Gly 110	Arg	Leu	
Lys	Ser	Phe 115	Ser '	Thr	Cys	Ala	Ser 120	His	Val	Thr	Val	Val 125	Thr	Met	Phe	
туг	Gly 130	Pro	Ala	Ile	Ile	Met 135	Tyr	Met	Arg	Pro	Gly 140	Ser	Trp	Tyr	Asp	
Pro 145	Glu	Trp	Asp	Lys	Lys 150	Val	Glu	Val	Leu	Tyr 155	Asn	Val	Ile	Ser	Ala 160	
Phe	Leu															
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gcc Ala	tgc Cys	atg Met	acc Thr 20	atg Met	gtg Val	ggc Gly	acc Thr	tcc Ser 25	tgg Trp	cto Leu	aca Thr	ggc	ato 11e 30	ato Ile	aca Thr	97
gcc Ala	acc Thr	acc Thr 35	cat His	gcc Ala	tcc Ser	ctc Leu	ato Ile 40	ttc Phe	tct Ser	cto Lev	rcc Pro	tto Phe 45	e ccc Pro	ago Ser	cac His	145
cca Pro	atg Met	atc Ile	cca Pro	cac His	ttt Phe	ctc Leu 55	tgt Cys	gac S Asp	ato Ile	ctç e Lei	g cca Pro 60	gta Val	a cto L Leu	g aga	ctg g Leu	193
gca Ala 65	agt Ser	gct Ala	gly aaa	aag Lys	cac His 70	agg Arg	agt Sei	gag Glu	g ato	tco Ser 75	gtg Val	g ato Met	g aca	a gct c Ala	acc Thr 80	241
gta Va]	gto Val	ttc Phe	atc Ile	atg Met	gtc Val	cct	tto Phe	c tct e Sei	t atq	g att	gto Val	ace L Thi	c tct r Sei	tac Tyi	atc r Ile	289

cgc atc ctg ggt gcc atc cta gca atg act tcc acc cag agc cgc cac Arg Ile Leu Gly Ala Ile Leu Ala Met Thr Ser Thr Gln Ser Arg His

aag gtc ttc tcc acc tgc tcc tcc cat ctg ctt gtg gtc tgt ctc ttc 385 Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Cys Leu Phe 115 120 125	
ttt gga aca gcc agc atc acc tac ata cgg ccc cag gca ggc tcc tct Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser 130 140	
gtc acc aca gac cgc atc ctc agt ctc ttc tac acg gtc atc aca ccc Val Thr Thr Asp Arg Ile Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro 145 150 155 160	
atg ctc Met Leu	
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Ala Cys Met Thr Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr 20 25 30	
Ala Thr Thr His Ala Ser Leu Ile Phe Ser Leu Pro Phe Pro Ser His 35 40 45	
Pro Met Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu 50 55 60	
Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr 65 70 75 80	
Val Val Phe Ile Met Val Pro Phe Ser Met Ile Val Thr Ser Tyr Ile 85 90 95	
Arg Ile Leu Gly Ala Ile Leu Ala Met Thr Ser Thr Gln Ser Arg His 100 105 110	
Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Cys Leu Phe 115 120 125	

Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser 130 135 140

Val	Thr	Thr	Asp	Arg	Ile	Leu	Ser	Leu	Phe	Tyr	$\mathtt{Thr}$	Val	Ile	$\mathtt{Thr}$	Pro
145					150					155					160

Met Leu

<pre> &lt;210&gt; 357 &lt;211&gt; 487 &lt;212&gt; DNA &lt;213&gt; Saimiri boliviensis  &lt;220&gt; &lt;221&gt; misc_feature &lt;222&gt; (1)(487) &lt;223&gt; Taxon = 27679; gene = SBO217; Accession DDBJ/EMBL/GenBank = AB</pre>	F179837
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gcc ttg acc cac aca ctc ctc atg gct cga ctg tcc ttc tgt gtg act Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr 35 40 45	145
ggg gaa att gct cac ttt ttc tgt gac atc act cct gtc ctg aag cta Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu 50 55 60	193
tca tgt tct gac acc cac atc aat gag atg atg gtt ttt gtc ttg gga Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly 65 70 75 80	241
ggc aca gta ctc atc atc ccc ttt cta tgc att gtc acc tcc tac atc Gly Thr Val Leu Ile Ile Pro Phe Leu Cys Ile Val Thr Ser Tyr Ile 85 90 95	289
tac att gtg cct gct att ctg agg gtc cga acc cat ggt ggg gcg ggc Tyr Ile Val Pro Ala Ile Leu Arg Val Arg Thr His Gly Gly Ala Gly 100 105 110	337
aag gcc ttt tcc acc tgc agt tcc cac ctc tgc att gtt tgt gtg ttc Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Val Phe 115 120 125	385
tat ggg acc ctc ttc agt gcc tac ctg tgt cct ccc tcc atc gcc tct Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser 130 135 140	433
gaa gat aag gac att gca aca gct gca atg tat acc ata gtg act ccc Glu Asp Lys Asp Ile Ala Thr Ala Ala Met Tyr Thr Ile Val Thr Pro 145 150 155 160	481
acg ttg Thr Leu	487

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Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr
Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
Gly Thr Val Leu Ile Ile Pro Phe Leu Cys Ile Val Thr Ser Tyr Ile
Tyr Ile Val Pro Ala Ile Leu Arg Val Arg Thr His Gly Gly Ala Gly
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Val Phe
Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser
                         135
Glu Asp Lys Asp Ile Ala Thr Ala Ala Met Tyr Thr Ile Val Thr Pro
 Thr Leu
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Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln
                                                                                 49
gtg tgc ttg ctc ctt ttg ttg ggt gtc tat ggg atg ggg gtt ttg ggg
Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly
                                                                                 97
gct gtg gct cat atg gga aac ata atg ttt atg acc ttt tgt tca gaa
                                                                                145
Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu
aat ctt gtc aat cac tac atg tgt gat gtc ctt ccc ctc ctt gag ctc
                                                                                193
Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu
     50
                                                                                241
tee tge aac age tet tae ata aat ttg etg ttg gtt ttt att att gtg
Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val
                       70
gcc att ggc att ggg gtg cca att gtc acc att ttt atc tct tat ggt Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly
                                                                                289
ttt att ctt tcc agc att ctc cac att agc tcc aca gag ggc agg tct
                                                                                337
Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser
              100
aaa gcc ttc agt acc tgc agc tcc cac ata att gtg gta tcg ctt ttc
                                                                                385
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe
                                120
          115
ttt ggg tca gga gct ttt atg tac ctc aaa cca cct tct att cta ccc
                                                                                 433
Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
                            135
     130
ctg gac cag ggg aaa gtg tct tcc att ttt tat act gca gtg gtg cca
                                                                                 481
Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro
                        150
 145
                                                                                 486
 tgt tt
 Cys
 <210> 360
 <211> 161
 <212>
         PRT
         Saimiri boliviensis
 <213>
 <220>
         misc_feature
 <221>
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         Taxon = 27679; gene = SBO218; Accession DDBJ/EMBL/GenBank = AF179838
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Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln
                                   10
Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly
                                25
Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu
Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu
Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val
Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly
                85
Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser
                                105
            100
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe
                            120
        115
Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro
Cys
<210> 361
<211> 487
<212> DNA
<213> Saimiri boliviensis
<220>
<221> misc feature
<222> (1)..(487)
<223> Taxon = 27679; gene = SB0219; Accession DDBJ/EMBL/GenBank = AF179839
<220>
<221> CDS
 <222> (2)..(487)
<223> Product = olfactory receptor
 t gtg gcc att tgc cac cct ctt caa tac tca gtc atc atg acc aca ggt
                                                                       49
  Val Ala Ile Cys His Pro Leu Gln Tyr Ser Val Ile Met Thr Thr Gly
```

tac tgt gga cag ctg gtg gct ttc tct tac atg agt ggt ttc atg atc Tyr Cys Gly Gln Leu Val Ala Phe Ser Tyr Met Ser Gly Phe Met Ile

10

20 tct gtc atc aag gtc tat ttc att tca cat gtt gct ttc tgt ggc tcc 145 Ser Val Ile Lys Val Tyr Phe Ile Ser His Val Ala Phe Cys Gly Ser aat gtt atg aac ctc ttt ttc tgt gat atc tca cca gtc cta aaa ctg 193 Asn Val Met Asn Leu Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu 55 gca tgc aaa gac atg tcc aca gct gag cta gtg gac ttt gct tta gct Ala Cys Lys Asp Met Ser Thr Ala Glu Leu Val Asp Phe Ala Leu Ala 241 70 atc gtc att ctt gtg atc cct ctc att acc act atc ctc tcc tat atc 289 Ile Val Ile Leu Val Ile Pro Leu Ile Thr Thr Ile Leu Ser Tyr Ile 85 tac att gtc tcc gcc att ctg cat ata ccc tcc acc cag gga agg aag 337 Tyr Ile Val Ser Ala Ile Leu His Ile Pro Ser Thr Gln Gly Arg Lys 100 105 aag gcc ttc tcc acc tgt gca tct cac ctc act gta gtc ata att ttt 385 Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe 120 tac aca gcc atg att ttt aca tat gtt cgg ccc aga gct att gca tca 433 Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser 140 135 ttt aat tcc aac aaa cta atc tca gct gtc tat gca gtc ctc aca ccc 481 Phe Asn Ser Asn Lys Leu Ile Ser Ala Val Tyr Ala Val Leu Thr Pro 487 atg cta Met Leu <210> 362 <211> 162 <212> PRT Saimiri boliviensis <213>

<220>

misc\_feature <221>

<222> (1)..(487)

Taxon = 27679; gene = SBO219; Accession DDBJ/EMBL/GenBank = AF179839

<400> 362

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Tyr Cys Gly Gln Leu Val Ala Phe Ser Tyr Met Ser Gly Phe Met Ile 25

Ser Val Ile Lys Val Tyr Phe Ile Ser His Val Ala Phe Cys Gly Ser

Asn Val Met Asn Leu Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu

Ala Cys Lys Asp Met Ser Thr Ala Glu Leu Val Asp Phe Ala Leu Ala Ile Val Ile Leu Val Ile Pro Leu Ile Thr Thr Ile Leu Ser Tyr Ile 90 Tyr Ile Val Ser Ala Ile Leu His Ile Pro Ser Thr Gln Gly Arg Lys 105 110 Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser 130 135 Phe Asn Ser Asn Lys Leu Ile Ser Ala Val Tyr Ala Val Leu Thr Pro 155 145 Met Leu <210> 363 488 <211> DNA <212> <213> Saimiri boliviensis <220> <221> misc\_feature (1)..(488)<222> <223> Taxon = 27679; gene = SBO220; pseudogene; Accession DDBJ/EMBL/GenBank = AF179840 <400> 363 tgtggccatc tgtaagcccc tgcattacac caccatcatg agcagcaaaa tctgcctgca 60 gettgtgett gggtgetggg ttettggttt teteateate ttteeaceae teetettagg 120 actaaatett gaettetgtg eetecaaegt egttgateat ttetaetgtg acaetateee 180 gctcctgcag atttcctgca cagacacgca gctcctggag aggatgggat tcatctcagc 240 gctggtgaca ctcttagtca cattggtaat ggtgataata tcatatactt atattgccct 300 gacaattcta aaaatccctt caactagtca gaggaaaaag gctttttcca cgtgttcttc 360 tcacatgatt gtgatatccc tttcttatgg cagctgccat cttcatgtat gttaagccat 420

<210> 364 <211> 487 <212> DNA <213> Saimiri boliviensis

<220>

cacttttg

480 488

cagtcaaaca aagggtatct ttttcaaagg gaatttcggt gctcaatacc tctgttgctc

<400> 365

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<223> Taxon = 27679; gene = SBO221; Accession DDBJ/EMBL/GenBank = AF179841
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<221> CDS
      (2)..(487)
<222>
<223> Product = olfactory receptor
<400> 364
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                                                                       49
 Val Ala Ile Cys Leu Pro Leu His Tyr Ala Thr Ile Met Ser Pro Met
                                                                       97
ctg tct cgc tcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat
Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
            20
gcc atg ttg cac act tta ctc ata gcc agg ttg cgt ttt tgt gca gac
                                                                      145
Ala Met Leu His Thr Leu Leu Ile Ala Arg Leu Arg Phe Cys Ala Asp
                            40
                                                                      193
aat gtg atc ttc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg
Asn Val Ile Phe His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
gcc tgc tct gac act cga gtt aat gaa ttg gtg ata ttt atc atg gga
                                                                      241
Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
                    70
ggc ctc att ctt gtc atc cca ttt cta ctt atc att ggg tcc tac gca
                                                                      289
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala
cga att gtc ttc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc
                                                                      337
Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
            100
                                105
aag gcc gtc tct act tgt ggc tcc cac ctc tct gtg gtg tca ctg ttc
                                                                      385
Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
        115
tat ggg act gtt att ggt ctc tac tta tgc cca tca gct aat aat tct
                                                                      433
Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser
                         135
act cta aag gag act gtc atg gct gtg atg tac act gtg atg gcc ccc
                                                                      481
Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro
                    150
                                                                       487
atg ctg
Met Leu
<210> 365
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Val Ala Ile Cys Leu Pro Leu His Tyr Ala Thr Ile Met Ser Pro Met
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Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His 25

Ala Met Leu His Thr Leu Leu Ile Ala Arg Leu Arg Phe Cys Ala Asp

Asn Val Ile Phe His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu

Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly 70

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala

Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys

Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 115

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser 135 130

Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro 155 150 145

Met Leu

<210> 366

<211> 487

DNA <212>

<213> Saimiri boliviensis

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<221> misc\_feature

<222> (1)..(487)

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<221> CDS

(2)..(487) <222>

<223> Product = olfactory receptor

<400> 366

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gtg tgt ttg ctc ctt ttg ttg ggt gtc tat ggg atg ggg gtt ttg ggg

Val C	ys :		Leu 20	Leu	Leu	Leu	Gly	Val 25	Tyr	Gly	Met	Gly	Val 30	Leu	Gly	
gct g Ala V	al.	gct Ala 35	cat His	aca Thr	gga Gly	aat Asn	ata Ile 40	gtg Val	ttt Phe	cta Leu	acc Thr	ttt Phe 45	tgt Cys	gca Ala	ggc Gly	145
aac c Asn L	eu	gtc Val	aat Asn	cac His	tac Tyr	atg Met 55	tgt Cys	gac Asp	atc Ile	ctt Leu	ccc Pro 60	ctt Leu	ctt Leu	gag Glu	ctc Leu	193
tcc to Ser C	gc gc	aat Asn	ggc Gly	tct Ser	tac Tyr 70	ata Ile	aat Asn	gtt Val	ctg Leu	gtc Val 75	atc Ile	ttt Phe	att Ile	gtt Val	gtg Val 80	241
acc a Thr I	tt 1e	ggc Gly	att Ile	999 Gly 85	gtg Val	ccc Pro	att Ile	gtt Val	gcc Ala 90	att Ile	ttt Phe	atc Ile	tct Ser	tat Tyr 95	ggt Gly	289
ttt a Phe I	tt le	ctt Leu	tcc Ser 100	agc Ser	aat Asn	ctc Leu	cac His	att Ile 105	agt Ser	tct Ser	gct Ala	gag Glu	ggc Gly 110	agg Arg	tct Ser	337
aaa g Lys A	gcc Ala	ttc Phe 115	agt Ser	acc Thr	tgc Cys	agc Ser	tcc Ser 120	cac His	ata Ile	att Ile	gca Ala	gtt Val 125	tct Ser	ctt Leu	ttc Phe	385
ttc g Phe G 1	130 31 y 399	tca Ser	gga Gly	gct Ala	ttt Phe	atg Met 135	tac Tyr	ctc Leu	aaa Lys	ccc Pro	tct Ser 140	tcc Ser	gtt Val	tta Leu	ccc Pro	433
ctg g Leu A 145	gac Asp	cag Gln	ggg Gly	aaa Lys	gta Val 150	Ser	tcc Ser	ctg Leu	ttt Phe	tat Tyr 155	Thr	att Ile	gtg Val	gtg Val	ccc Pro 160	481
atg t Met F																487
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<220: <221: <222: <223:	> 1	(1)	-//0	ture 7) 2767		ene,	= SE	30222	:; Ac	cess	sion	DDBJ	r/EME	BL/Ge	enBank	: = AF179842
<400	>	367														
Val 1	Ala	Ile	Сув	Asr 5	n Pro	Let	Leu	туг	Met 10	: Val	L Thr	. Met	Se1	15	Gln	
Val	Cys	Leu	Let 20	ı Lev	ı Leı	ı Leı	ı Gly	y Val 25	L Туз	c Gly	/ Met	: Gly	7 Val 30	l Lei	ı Gly	
Ala	Val	Ala 35	a His	s Thi	r Gly	y Ası	1 Ile 40	e Val	l Phe	e Lei	ı Thi	r Phe	e Cy	s Ala	a Gly	
	Leu 50	. Val	l Ası	n His	з Ту:	r Me	Cy:	s As	o Il	e Le	u Pro 60	o Le	ı Le	u Gl	u Leu	

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Ser Cys Asn Gly Ser Tyr Ile Asn Val Leu Val Ile Phe Ile Val Val
                     70
Thr Ile Gly Ile Gly Val Pro Ile Val Ala Ile Phe Ile Ser Tyr Gly
Phe Ile Leu Ser Ser Asn Leu His Ile Ser Ser Ala Glu Gly Arg Ser
                                 105
            100
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Ala Val Ser Leu Phe
                             120
Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Ser Ser Val Leu Pro
Leu Asp Gln Gly Lys Val Ser Ser Leu Phe Tyr Thr Ile Val Val Pro
                                          155
                                                                160
Met Phe
<210> 368
       487
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<212>
       DNA
<213> Saimiri boliviensis
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       (2)..(487)
<222>
       Product = olfactory receptor
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                                                                           49
  Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg
                                                                           97
ctg tgt gga ctg ctg gtt ctg gca tcc tgg atc ctg agt gcc ctg aat
Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
             20
                                  25
tcc tca tta caa acc tta ata gtg ctg cgg ctt tcc ttc tgc aca gac
                                                                          145
Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp
         35
                              40
                                                                          193
ttg gaa atc ccc cac ttt ttc tgc gaa ctt aat cag gtc ata cat ctt
Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu
gcc tgt tat gac act ttc ctt aat gat gtg gtg atg tat ttg gca gct Ala Cys Tyr Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala
                                                                          241
                                           75
                      70
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atg ctg ctg ggc ggt ggt ccc ctc aca gga att att ta Met Leu Leu Gly Gly Gly Pro Leu Thr Gly Ile Ile Ty 85 90	c tct tac tct 289 r Ser Tyr Ser 95
aag ata gtt tcc tcc ata cgt gca atc tca tca gct ca Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gl 100 105	g ggg aag tac 337 n Gly Lys Tyr 110
aag gcg ttt tcc acc tgt gca tct cac atc tta att gt Lys Ala Phe Ser Thr Cys Ala Ser His Ile Leu Ile Va 115 120 12	l Ser Leu Phe
tat ggt aca ctc cta ggt gtg tac ctt agt tct gct gc Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Al 130	a act ggc aac 433 a Thr Gly Asn
tca cat tca agt gct gca gcc ttg gtg atg tac act gt Ser His Ser Ser Ala Ala Ala Leu Val Met Tyr Thr Va 145 150 155	g gtc acc ccc 481 1 Val Thr Pro 160
atg ctg Met Leu	487
<210> 369 <211> 162 <212> PRT <213> Saimiri boliviensis <220> <221> misc feature	
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<pre>&lt;222&gt; (1)(487) &lt;223&gt; Taxon = 27679; gene = SBO223; Accession DDE &lt;400&gt; 369  Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Il</pre>	le Asn Pro Arg 15
<pre>&lt;222&gt; (1)(487) &lt;223&gt; Taxon = 27679; gene = SBO223; Accession DDE &lt;400&gt; 369  Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr II 1</pre>	le Asn Pro Arg 15 er Ala Leu Asn 30 he Cys Thr Asp
<pre> &lt;222&gt; (1)(487) &lt;223&gt; Taxon = 27679; gene = SBO223; Accession DDE  &lt;400&gt; 369  Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr II 1</pre>	le Asn Pro Arg 15  er Ala Leu Asn 30  he Cys Thr Asp
<pre> &lt;222&gt; (1)(487) &lt;223&gt; Taxon = 27679; gene = SBO223; Accession DDE  &lt;400&gt; 369  Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr II 1</pre>	le Asn Pro Arg 15  er Ala Leu Asn 30  he Cys Thr Asp 5
<pre> &lt;222&gt; (1)(487) &lt;223&gt; Taxon = 27679; gene = SBO223; Accession DDE  &lt;400&gt; 369  Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr II 1</pre>	le Asn Pro Arg 15  er Ala Leu Asn 30  he Cys Thr Asp 5  al Ile His Leu  yr Leu Ala Ala 80

Lys Ala Phe Ser Thr Cys Ala Ser His Ile Leu Ile Val Ser Leu Phe



Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn

Ser His Ser Ser Ala Ala Ala Leu Val Met Tyr Thr Val Val Thr Pro 155

Met Leu

<210>	370
<211>	649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc\_feature

(1)..(649)

<223> Taxon = 10092; clone = OR1-72M15; Accession DDBJ/EMBL/GenBank = AF073959

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 370

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C	ala	get	yac	acc	990	-1	m1 -	2	mb	mb	T10	Dro	T.376	Val	Leu	Gln	
	Ile	Ala	Asp	Ile	Gly	Phe	Thr	Ser	THE	TIII	TTE	PIO	цуз	Val	15	·	
	1				5					10					15		

97 act atc cac aca cag agc aaa ttc atc tct ttc tcg ggc tgc atc aca Thr Ile His Thr Gln Ser Lys Phe Ile Ser Phe Ser Gly Cys Ile Thr 20 25

cag ata ttt ttc ttc att gtg ttt gga tgc ctg gac aat tta ctc cta 145 Gln Ile Phe Phe Phe Ile Val Phe Gly Cys Leu Asp Asn Leu Leu

tca gtg atg gcc tat gac cgc ttt gtg gcc atc tgc cat ccc ttg cac 193 Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50

tat gtg gtc atc atg aat tot tgc ttc tgt gtg atg ctg gct ctt gga 241 Tyr Val Val Ile Met Asn Ser Cys Phe Cys Val Met Leu Ala Leu Gly

tca tgg ata gtc agc gtc atg agt tcc cta cct gag acc ttg act gtg 289 Ser Trp Ile Val Ser Val Met Ser Ser Leu Pro Glu Thr Leu Thr Val 90

337 tta aga cta tcc ttc tgt aca aac atg gaa att cca cac ttt ttc tgt Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys 105 100

gat ctt ccc gaa gtc ctg aag ctt gcc tgt tct gac acc ctt gtt aat 385 Asp Leu Pro Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Leu Val Asn 115

aac att gtg aca tat tot ata acc ata gtc ata gct ggt ttc cca ttc



Asn Ile Val Thr Tyr Ser Ile Thr Ile Val Ile Ala Gly Phe Pro Phe 130 140	
tct ggg att cta ttg tct tat tct aag att ttc tcc tcc atc cta aga Ser Gly Ile Leu Leu Ser Tyr Ser Lys Ile Phe Ser Ser Ile Leu Arg 145 150 155 160	481
att cct tca gct ggg ggc aag tac aaa gcc ttt tct acc tgt ggg tct Ile Pro Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175	529
cat ctt ttg gtg gtc ttc tta ttc tat agc aat ggt ctt ggg gtc tac His Leu Leu Val Val Phe Leu Phe Tyr Ser Asn Gly Leu Gly Val Tyr 180 185 190	577
ctc agc tct gca gcc aca tca tct tct aga atg agt cta gtt gcc tca Leu Ser Ser Ala Ala Thr Ser Ser Ser Arg Met Ser Leu Val Ala Ser 195 200 205	625
ctg atg tac agc ata gtc act ccc Leu Met Tyr Ser Ile Val Thr Pro 210 215	649
<210> 371 <211> 216	
<212> PRT <213> Mus musculus domesticus	
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MEU ( ) 7 1 7	
AF073959 <400> 371	
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<pre>&lt;400&gt; 371  Ile Ala Asp Ile Gly Phe Thr Ser Thr Thr Ile Pro Lys Val Leu Gln 1</pre>	
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<pre>&lt;400&gt; 371  Ile Ala Asp Ile Gly Phe Thr Ser Thr Thr Ile Pro Lys Val Leu Gln 1</pre>	

115 120 125

Asn Ile Val Thr Tyr Ser Ile Thr Ile Val Ile Ala Gly Phe Pro Phe Ser Gly Ile Leu Leu Ser Tyr Ser Lys Ile Phe Ser Ser Ile Leu Arg Ile Pro Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser 165 His Leu Leu Val Val Phe Leu Phe Tyr Ser Asn Gly Leu Gly Val Tyr 185 180 Leu Ser Ser Ala Ala Thr Ser Ser Ser Arg Met Ser Leu Val Ala Ser 200 Leu Met Tyr Ser Ile Val Thr Pro <210> 372 <211> 649 <212> DNA <213> Mus musculus domesticus <220> <221> misc\_feature <222> (1)..(649) <223> Taxon = 10092; clone = OR1-72M16; Accession DDBJ/EMBL/GenBank = AF073960 <220> <221> CDS <222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7 <400> 372 c ttc tct gac ttc tgc ttt tcc tct gtg acc att ccc aaa ttg ctg cag Phe Ser Asp Phe Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln 49 97 aac atg caa agc caa gtt cca tcc ata ccc tat gca ggt tgc ctg gca Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala 145 caa atg tac ttt ttc ctg ctt ttt gca gat ctc gag agc ttc ctc ctt Gln Met Tyr Phe Phe Leu Leu Phe Ala Asp Leu Glu Ser Phe Leu Leu 40 gtg gcc atg gcc tat gat cgc tat gtg gcc atc tgc ttc ccc cta cac 193 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 60 tat act age ate atg age eec aag etg tgt etc tge etg gtg gea eta Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Leu Cys Leu Val Ala Leu 70

tct tgg cta ctg acc aca gtc atc tct ttg tca cac aca ctg ctc atg

Ser	Trp	Leu	Leu	Thr 85	Thr	Val	Ile	Ser	Leu 90	Ser	His	Thr	Leu	Leu 95	Met	
gct Ala	cgg Arg	ctc Leu	tcc Ser 100	ttc Phe	tgt Cys	gct Ala	aac Asn	aat Asn 105	gtg Val	att Ile	cct Pro	cac His	ttt Phe 110	ttc Phe	tgt Cys	337
gat Asp	atg Met	tca Ser 115	gct Ala	ctt Leu	ctg Leu	aag Lys	tta Leu 120	gcc Ala	tgc Cys	tct Ser	gac Asp	att Ile 125	cag Gln	atc Ile	aat Asn	385
aag Lys	ttg Leu 130	atg Met	ata Ile	ttt Phe	atc Ile	ttg Leu 135	gga Gly	gga Gly	ctt Leu	gtc Val	att Ile 140	att Ile	gtc Val	cca Pro	ttc Phe	433
ctg Leu 145	ctg Leu	ata Ile	ttt Phe	tca Ser	tcc Ser 150	tat Tyr	gca Ala	cga Arg	ata Ile	gtg Val 155	tcc Ser	tcc Ser	att Ile	ctc Leu	aag Lys 160	481
gtc Val	ccc Pro	tct Ser	tct Ser	aga Arg 165	agc Ser	atc Ile	cgc Arg	aag Lys	gcc Ala 170	ttc Phe	tcc Ser	acc Thr	tgt Cys	ggt Gly 175	tcc Ser	529
cac His	ctc Leu	tct Ser	gtg Val 180	gtg Val	tct Ser	ctt Leu	ttc Phe	tat Tyr 185	Gly aaa	aca Thr	atc Ile	att Ile	ggt Gly 190	ctc Leu	tat Tyr	577
tta Leu	cgt Arg	cca Pro 195	tca Ser	gct Ala	aat Asn	aat Asn	tca Ser 200	acc Thr	att Ile	aag Lys	gag Glu	act Thr 205	gtc Val	atg Met	gct Ala	625
gtg Val	atg Met 210	Tyr	acg Thr	gtg Val	gtg Val	acc Thr 215	cct Pro									649
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Phe 1	Ser	Asp	Phe	Cys 5	Phe	Ser	Ser	Val	Thr 10	Ile	Pro	Lys	Leu	Leu 15	Gln	
Asn	Met	Gln	Ser 20	Gln	Val	Pro	Ser	Ile 25	Pro	Tyr	Ala	Gly	Cys	Leu	Ala	
Gln	. Met	Tyr 35	Phe	. Phe	. Leu	Leu	Phe 40	. Ala	Asp	Leu	Glu	Ser 45	Phe	. Leu	. Leu	
Val	. Ala	. Met	. Ala	туг	Asp	Arg 55	Tyr	· Val	Ala	ı Ile	: Сув 60	Phe	Prc	Leu	ı His	
-	- Thr	- Ser	- Ile	. Met	: Ser	Pro	Lys	. Leu	і Суя	Lev	ι Суя	. Le	ı Val	Ala	a Leu	

Ser Trp Leu Leu Thr Thr Val Ile Ser Leu Ser His Thr Leu Leu Met

75

Ala Arg Leu Ser Phe Cys Ala Asn Asn Val Ile Pro His Phe Phe Cys

Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile Gln Ile Asn

Lys Leu Met Ile Phe Ile Leu Gly Gly Leu Val Ile Ile Val Pro Phe 130

Leu Leu Ile Phe Ser Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys 150

Val Pro Ser Ser Arg Ser Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser 170

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 185

Leu Arg Pro Ser Ala Asn Asn Ser Thr Ile Lys Glu Thr Val Met Ala 205

Val Met Tyr Thr Val Val Thr Pro

<210> 374

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc\_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR10M; Accession DDBJ/EMBL/GenBank = AF073961

<220>

<221> CDS

<222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 374

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97 aac atg cag agc cag. gac tca tcc atc acc tat gca gga tgc ctg aca Asn Met Gln Ser Gln Asp Ser Ser Ile Thr Tyr Ala Gly Cys Leu Thr 25

caa atg tac ttt ttc ttg ctc ttt gga gac ctt gag agc ttc ctc ctt 145 Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu

35 40 gtg gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc ccc ctt cat 193 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 55 241 tac atg agc atc atg agc ccc agc ctc tgt gtg agt ctg gtg ctg ctg Tyr Met Ser Ile Met Ser Pro Ser Leu Cys Val Ser Leu Val Leu Leu 75 tcc tgg gtg ctg acc act ttc cat gcc atg ctg cat acc ctg ctc atg 289 Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met 90 gcc aga ttg tca ttc tgt gag gac aat gtg atc ccc cac ttt ttc tgt Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys 337 100 gac atg tct gct ctg ctg aag ctg tcc tgc tct gac act cac gtt aat 385 Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn 120 gaa ttg gtg ata ttt gtc aca gga ggc ctg atc ctt gtc att cca ttt 433 Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Ile Pro Phe 135 gtg ctc atc ctt gtg tcc tat gca cga att gtg tcc tcc att ctc aag 481 Val Leu Ile Leu Val Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys 155 150 gtc ccg tct gct cga ggc atc cgt aaa gcc ttc tcc acc tgt ggg tcc 529 Val Pro Ser Ala Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser cac ctg tct gtg gtg tca ctg ttc tat ggg gca atc att ggt ctg tac 577 His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Ile Ile Gly Leu Tyr 190 180 625 tta tgt cca tca gct gat aac tct act gtg aag gaa act gtc atg gcc Leu Cys Pro Ser Ala Asp Asn Ser Thr Val Lys Glu Thr Val Met Ala 205 200 195 649 atg atg tac aca gtg gtg act ccc Met Met Tyr Thr Val Val Thr Pro 210 <210> 375 <211> 216 <212> Mus musculus domesticus <213> <220> <221> misc\_feature (1)..(649) Taxon = 10092; clone = OR10M; Accession DDBJ/EMBL/GenBank = AF073961 <223> <400> 375

Asn Met Gln Ser Gln Asp Ser Ser Ile Thr Tyr Ala Gly Cys Leu Thr

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln

Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 55

Tyr Met Ser Ile Met Ser Pro Ser Leu Cys Val Ser Leu Val Leu Leu

Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met

Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys

Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn

Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Ile Pro Phe 130

Val Leu Ile Leu Val Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys 150

Val Pro Ser Ala Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser 165

His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Ile Ile Gly Leu Tyr

Leu Cys Pro Ser Ala Asp Asn Ser Thr Val Lys Glu Thr Val Met Ala 200

Met Met Tyr Thr Val Val Thr Pro 210

<210> 376

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc\_feature

(1)..(649)

<223> Taxon = 10092; clone = OR11M; Accession DDBJ/EMBL/GenBank = AF073962

<220>

<221> CDS

(2)..(649) <222>

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 376

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aat atg o Asn Met G	ag agc Sln Ser 20	cag ga Gln As	c cca p Pro	tcc Ser	atc Ile 25	ccc Pro	tat Tyr	gga Gly	ggt Gly	tgc Cys 30	ctg Leu	gca Ala	97
caa ata t Gln Ile P 3	tc ttc Phe Phe 35	ttt at Phe Me	g ctt t Leu	ttt Phe 40	gga Gly	gac Asp	atg Met	gaa Glu	agc Ser 45	ttc Phe	ctt Leu	ctt Leu	145
gta gcc a Val Ala M 50	atg gcc Met Ala	tat ga Tyr As	c cgc p Arg 55	tat Tyr	gtg Val	gcc Ala	atc Ile	tgc Cys 60	ttc Phe	cct Pro	ctg Leu	cat His	193
tac act a Tyr Thr S 65	agc atc Ser Ile	atg ag Met Se 70	t cct r Pro	aag Lys	gtc Val	tgt Cys	act Thr 75	ttt Phe	cta Leu	gtg Val	cta Leu	ctg Leu 80	241
ttg tgg a Leu Trp I	ata ctg Ile Leu	aca ac Thr Th 85	a cca r Pro	cat His	gcc Ala	aca Thr 90	atg Met	caa Gln	att Ile	ctg Leu	ctc Leu 95	aca Thr	289
gta aga d Val Arg I	ctg tct Leu Ser 100	ttt tg Phe Cy	t gag s Glu	aac Asn	aat Asn 105	gtg Val	ttt Phe	ctc Leu	aac Asn	ttt Phe 110	ttc Phe	tgt Cys	337
gac ata t Asp Ile I	ttt gtt Phe Val 115	ctc tt Leu Le	a aag u Lys	ctg Leu 120	gcc Ala	tgc Cys	tca Ser	gac Asp	act Thr 125	tat Tyr	gtt Val	aat Asn	385
gat ttg a Asp Leu M 130	atg ata Met Ile	ctt at Leu Il	c atg e Met 135	gga Gly	Glà aaa	ctc Leu	atc Ile	att Ile 140	gtt Val	att Ile	cca Pro	ttc Phe	433
ctg ctc a Leu Leu 1 145	att gtt Ile Val	ata to Ile Se	r Tyr	gca Ala	agg Arg	atc Ile	atc Ile 155	tcc Ser	tct Ser	act Thr	ctt Leu	aag Lys 160	481
gtt cca Val Pro	tct act Ser Thr	caa gg Gln Gl 165	c atc y Ile	cac His	aag Lys	gtc Val 170	ttc Phe	tct Ser	acc Thr	tgt Cys	ggc Gly 175	tct Ser	529
cat ctg	tct gtg Ser Val 180	Val Se	t ctg r Leu	ttc Phe	tat Tyr 185	Gly aaa	aca Thr	att Ile	att Ile	ggt Gly 190	ctc Leu	tac Tyr	577
tta tgt Leu Cys	cca tca Pro Ser 195	ggt aa Gly As	it aat sn Asn	ttc Phe 200	Ser	cta Leu	aag Lys	gjà aaa	tct Ser 205	gcc Ala	atg Met	gct Ala	625
atg atg Met Met 210	tac aca Tyr Thr	gtg gt Val Va	g act il Thr 215	Pro									649
<211> 2 <212> P	77 216 PRT Mus musc	ulus d	omesti	.cus									
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Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln

Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Gly Gly Cys Leu Ala

Gln Ile Phe Phe Phe Met Leu Phe Gly Asp Met Glu Ser Phe Leu Leu

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50

Tyr Thr Ser Ile Met Ser Pro Lys Val Cys Thr Phe Leu Val Leu Leu

Leu Trp Ile Leu Thr Thr Pro His Ala Thr Met Gln Ile Leu Leu Thr

Val Arg Leu Ser Phe Cys Glu Asn Asn Val Phe Leu Asn Phe Phe Cys

Asp Ile Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn 125

Asp Leu Met Ile Leu Ile Met Gly Gly Leu Ile Ile Val Ile Pro Phe

Leu Leu Ile Val Ile Ser Tyr Ala Arg Ile Ile Ser Ser Thr Leu Lys 145

Val Pro Ser Thr Gln Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr

Leu Cys Pro Ser Gly Asn Asn Phe Ser Leu Lys Gly Ser Ala Met Ala 200 195

Met Met Tyr Thr Val Val Thr Pro 215 210

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<220>

<221> misc\_feature

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<220> <221> CDS <222> (2)(649) <223> Product = olfactory receptor; region between transmembrane domain TM2 and TM7	.ns
<pre>&lt;400&gt; 378 c ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aag ttg cta cag Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln 1 5 10 15</pre>	19 .
aac atg cag agc cag gac acg tcc atc tcc tat gct ggc tgt ctg aca Asn Met Gln Ser Gln Asp Thr Ser Ile Ser Tyr Ala Gly Cys Leu Thr 20 25 30	97
caa atg tac ttt tta ttg gtt ttt gga gac ctg gag agc atc ctt ctt Gln Met Tyr Phe Leu Leu Val Phe Gly Asp Leu Glu Ser Ile Leu Leu 35 40 45	<u> 1</u> 5
ttg gtc atg gct tat gac cgg tat gtg gct gtc tgc ttc ccc ctt cat Leu Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Phe Pro Leu His 50 55 60	)3
tac atg agc atc atg agc ccc aca ctc tgt gtg tgt ctg cta gtg tta  Tyr Met Ser Ile Met Ser Pro Thr Leu Cys Val Cys Leu Leu Val Leu  65 70 75 80	11
tcc tgg gta ttt act gtg ctg tat tct atg ttg cac act cta ctc ttg  Ser Trp Val Phe Thr Val Leu Tyr Ser Met Leu His Thr Leu Leu  85  90  95	}9
tct aga ttg tca ttc tgt gag gat aac ttg atc cac cac ttt ttc tgt Ser Arg Leu Ser Phe Cys Glu Asp Asn Leu Ile His His Phe Phe Cys 100 105 110	37
gac ata tot goo otg otc aag ttg got tgo tot gac att cat att aat Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 115 120 125	35
gaa tta atg ata ttt atc atg gga ggg ctt gtt agc atc atc cca ttc Glu Leu Met Ile Phe Ile Met Gly Gly Leu Val Ser Ile Ile Pro Phe 130 135 140	33
tta ctc att gtt gtg tcc tat ata caa att gtc tac tcc att cta aag Leu Leu Ile Val Val Ser Tyr Ile Gln Ile Val Tyr Ser Ile Leu Lys 145 150 155 160	31
att tca tct gct cat gtt tta cac aag atc ttc tcc acc tgt ggg tcc 52  Ile Ser Ser Ala His Val Leu His Lys Ile Phe Ser Thr Cys Gly Ser  165 170 175	<u>.</u>
cac ctg tct gta gtc tca ctg ttc tat ggg aca att ttt gct ctc tac 57 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Phe Ala Leu Tyr 180 185 190	77
tta tgt cca tca gct aat aac tct act gtg aag gag att tcc atg gcc Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Ile Ser Met Ala 195 200 205	25
atg atg tgc aca gtg gtg act ccc  Met Met Cys Thr Val Val Thr Pro 210 215	19

<400> 379

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<210> 379
<211> 216
<212> PRT
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR12M; Accession DDBJ/EMBL/GenBank = AF073963
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Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Gln 1 5 10 15

Asn Met Gln Ser Gln Asp Thr Ser Ile Ser Tyr Ala Gly Cys Leu Thr 20 25 30

Gln Met Tyr Phe Leu Leu Val Phe Gly Asp Leu Glu Ser Ile Leu Leu 35 40 45

Leu Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Phe Pro Leu His 50 55 60

Tyr Met Ser Ile Met Ser Pro Thr Leu Cys Val Cys Leu Leu Val Leu 65 70 75 80

Ser Trp Val Phe Thr Val Leu Tyr Ser Met Leu His Thr Leu Leu Leu 85 90 95

Ser Arg Leu Ser Phe Cys Glu Asp Asn Leu Ile His His Phe Phe Cys
100 105 110

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 115 120 125

Glu Leu Met Ile Phe Ile Met Gly Gly Leu Val Ser Ile Ile Pro Phe 130 135 140

Leu Leu Ile Val Val Ser Tyr Ile Gln Ile Val Tyr Ser Ile Leu Lys 145 150 155 160

Ile Ser Ser Ala His Val Leu His Lys Ile Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Phe Ala Leu Tyr 180 185 190

Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Ile Ser Met Ala 195 200 205

Met Met Cys Thr Val Val Thr Pro

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<210> 380
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<212> DNA
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<221> CDS
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<223> Product = olfactory receptor; region between transmembrane domains
TM2 and TM7
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  Phe Ser Asp Ile Gly Phe Ile Ser Thr Thr Ile Pro Lys Met Leu Val
aat atc caa aca cag agc aag tcc atc tcc tat gca gaa tgc atc acc
                                                                          97
Asn Ile Gln Thr Gln Ser Lys Ser Ile Ser Tyr Ala Glu Cys Ile Thr
            20
                                                                         145
cag att tat ttt ttc atg ctc ttt gga ggc atg gac ata ctt ctc ctc
Gln Ile Tyr Phe Phe Met Leu Phe Gly Gly Met Asp Ile Leu Leu
acc gtg atg gcc tat gac cga ttt gtg gcc atc tgt cac ccc ctt cac
                                                                         193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
                                                                         241
tat tca gtc att atg aat ccc caa cta agt ggc ttg ctg gtt ctt gta
Tyr Ser Val Ile Met Asn Pro Gln Leu Ser Gly Leu Leu Val Leu Val
tca tgg ttt att agc ttt tca tat tct ctg ata cag agt cta ttg atg
                                                                          289
Ser Trp Phe Ile Ser Phe Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
                 85
ctg cgg ttg tcc ttc tgt aca aat cag ata att aaa cac ttt tac tgt
Leu Arg Leu Ser Phe Cys Thr Asn Gln Ile Ile Lys His Phe Tyr Cys
                                                                          337
                                  105
             100
gaa tat tot aga goo oto act ata goo tgo toa gao aca ota ato aat
                                                                          385
Glu Tyr Ser Arg Ala Leu Thr Ile Ala Cys Ser Asp Thr Leu Ile Asn
                              120
cat atc ctt ctt tat att ctg ata tgt gtc ctt ggc ttc atc cct ttc
                                                                          433
His Ile Leu Leu Tyr Ile Leu Ile Cys Val Leu Gly Phe Ile Pro Phe
                         135
                                               140
                                                                          481
tca ggg atc ctt tat tca tac tgt aaa att gtt tct tct att ttg aga
Ser Gly Ile Leu Tyr Ser Tyr Cys Lys Ile Val Ser Ser Ile Leu Arg
                                           155
                                                                          529
att cca tca aca gat gga aaa tat aaa gca ttt tct acc tgt ggg tct
Ile Pro Ser Thr Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
                 165
                                                                          577
cat cta tca gtg gtt tct tta ttc tat ggg aca ggc ctt ggt gtg tac
```

```
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
            180
                                  185
ctt agt tct gat gta act tcc tcc tct ggg aag gac gtg gtg gcc tca
Leu Ser Ser Asp Val Thr Ser Ser Gly Lys Asp Val Val Ala Ser
                                                                           625
                              200
                                                    205
                                                                           649
gta atg tat aca gtg gtc acc cct
Val Met Tyr Thr Val Val Thr Pro
    210
<210> 381
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AF073964
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Asn Ile Gln Thr Gln Ser Lys Ser Ile Ser Tyr Ala Glu Cys Ile Thr
Gln Ile Tyr Phe Phe Met Leu Phe Gly Gly Met Asp Ile Leu Leu
                               40
         35
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
Tyr Ser Val Ile Met Asn Pro Gln Leu Ser Gly Leu Leu Val Leu Val
Ser Trp Phe Ile Ser Phe Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
                                        90
Leu Arg Leu Ser Phe Cys Thr Asn Gln Ile Ile Lys His Phe Tyr Cys
                                                         110
Glu Tyr Ser Arg Ala Leu Thr Ile Ala Cys Ser Asp Thr Leu Ile Asn
                               120
         115
His Ile Leu Leu Tyr Ile Leu Ile Cys Val Leu Gly Phe Ile Pro Phe
 Ser Gly Ile Leu Tyr Ser Tyr Cys Lys Ile Val Ser Ser Ile Leu Arg
```

Ile Pro Ser Thr Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser

150

145

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr

Leu Ser Ser Asp Val Thr Ser Ser Gly Lys Asp Val Val Ala Ser

Val Met Tyr Thr Val Val Thr Pro

<210> 382

<211> 643 <212> DNA

<213> Mus musculus domesticus

<220>

<221> misc\_feature

<222> (1)..(643)

<223> Taxon = 10092; clone = OR15-71M20; Accession DDBJ/EMBL/GenBank = AF073965

<220>

<221> CDS

<222> (2)..(643)
<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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gac ctc cta tcg gcg aag aaa acc atc tca ata gaa ggc tgc ctg gct Asp Leu Leu Ser Ala Lys Lys Thr Ile Ser Ile Glu Gly Cys Leu Ala 20 .

cag gtc ttt ttt gtg ttt ttt cct tct ggt act gaa gcc tgc ctg ctc 145 Gln Val Phe Phe Val Phe Pro Ser Gly Thr Glu Ala Cys Leu Leu 35

tct gtc atg gct tat gac cgc tat gct gcc atc tgc cat ccc ctg ctc 193 Ser Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro Leu Leu 55

241 tac ggc cag gtg atg aga aat gag ttg tgt gta agg ctt gtg gtc atc Tyr Gly Gln Val Met Arg Asn Glu Leu Cys Val Arg Leu Val Val Ile

289 tca tgg ggc gtg gcc tct ctc aac gca acc atc atc gtg ctc ttg gct Ser Trp Gly Val Ala Ser Leu Asn Ala Thr Ile Ile Val Leu Leu Ala 90

gtc aac ctg gac ttc tgt ggg gct caa acc att cac cac tac acc tgt 337 Val Asn Leu Asp Phe Cys Gly Ala Gln Thr Ile His His Tyr Thr Cys

gag ctg cct gcc ctt ttc ccc ttg tcc tgt tcc gat atc tcc atc act 385 Glu Leu Pro Ala Leu Phe Pro Leu Ser Cys Ser Asp Ile Ser Ile Thr 120 115

433 gtc gtc gtc ctg ctt tgc tcc agc ttg ctg cat ggg ctg gga acc ttt

Val Val 1																
	al 1 30	Val	Leu	Leu	Суѕ	Ser 135	Ser	Leu	Leu	His	Gly 140	Leu	Gly	Thr	Phe	
atc co Ile P: 145	ct a	atc Ile	ttc Phe	ttc Phe	tcc Ser 150	tat Tyr	gcc Ala	cgc Arg	att Ile	gtc Val 155	tcc Ser	gcc Ala	atc Ile	ttg Leu	agc Ser 160	481
atc a	gt t er S	tcc Ser	acc Thr	acc Thr 165	Gly 999	agg Arg	agc Ser	aag Lys	gcc Ala 170	ttc Phe	tcc Ser	acc Thr	tgc Cys	tct Ser 175	tcc Ser	529
cac c His L	tc q	gct Ala	gca Ala 180	gtg Val	acc Thr	ttg Leu	ttc Phe	ttt Phe 185	Gly aaa	tct Ser	ggc Gly	ttt Phe	ctt Leu 190	tgc Cys	tat Tyr	577
ctc a Leu M	let 1	ccg Pro 195	cct Pro	tct Ser	ggt Gly	tct Ser	tct Ser 200	ctg Leu	gac Asp	ttg Leu	ctc Leu	ttg Leu 205	tcg Ser	ttg Leu	cag Gln	625
tac a Tyr S 2																643
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Phe V	/al	83 Asp		5					10					15		
Phe V 1	/al Leu Val	83 Asp Leu	Ser 20	5 Ala Val	Lys	Lys	Thr	Ile 25 Ser	Ser	Ile	Glu	Gly	Cys 30	Leu	Ala	
Phe V  1  Asp I  Gln V	/al Leu Val	83 Asp Leu Phe 35	Ser 20 Phe	5 Ala Val	Lys Phe	Lys Phe	Thr Pro	Ile 25 Ser	Ser	Ile	Glu	Gly Ala 45	Cys	Leu Leu	Ala Leu	
Phe V  1  Asp I  Gln V	Jal Leu Val Val	83 Asp Leu Phe 35 Met	Ser 20 Phe	Ala Val Tyr	Lys Phe Asp	Lys Phe Arg 55	Thr Pro 40	Ile 25 Ser	Ser Gly Ala	Ile Thr	Glu Glu Cys 60	Gly Ala 45	Cys 30 Cys	Leu Leu	Ala Leu Leu	
Phe Villamore Vi	Val Val Val So Gly	83 Asp Leu Phe 35 Met	Ser 20 Phe Ala Val	5 Ala Val Tyr	Lys Phe Asp Arg	Lys Phe Arg 55 Asn	Thr Pro 40 Tyr	Ile 25 Ser Ala	Ser Gly Ala	Ile Thr Ile	Glu Glu Cys 60	Gly Ala 45 His	Cys 30 Cys Pro	Leu Leu Leu Val	Ala Leu Leu Ile 80	
Phe Villamore Vi	Val Val Soly Trp	83 Asp Leu Phe 35 Met Gln	Ser 20 Phe Ala Val	Ala Val Tyr Met Ala 85	Lys Phe Asp Arg 70 Ser	Lys Phe Arg 55 Asn	Thr Pro 40 Tyr Glu	Ile 25 Ser Ala Leu	Ser Gly Ala Cys Thr	Thr Ile	Glu Glu Cys 60 Arg	Gly Ala 45 His	Cys 30 Cys Pro Val	Leu Leu Val Leu 95	Ala Leu Leu Ile 80	

115 120 125

Val	Val 130	Val	Leu	Leu	Cys	Ser 135	Ser	Leu	Leu	His	Gly 140	Leu	Gly	Thr	Phe	
Ile 145	Pro	Ile	Phe	Phe	Ser 150	Tyr	Ala	Arg	Ile	Val 155	Ser	Ala	Ile	Leu	Ser 160	
Ile	Ser	Ser	Thr	Thr 165	Gly	Arg	Ser	Lys	Ala 170	Phe	Ser	Thr	Cys	Ser 175	Ser	
His	Leu	Ala	Ala 180	Val	Thr	Leu	Phe	Phe 185	Gly	Ser	Gly	Phe	Leu 190	Cys	Tyr	
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Tyr	Ser 210	Ala	Val	Thr	Pro											
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aac Asn	cat His	ctc Leu	cta Leu 20	ggt Gly	agc Ser	aag Lys	gcc Ala	atc Ile 25	tcc Ser	ttt Phe	ggg Gly	gga Gly	tgt Cys 30	atg Met	gca Ala	97
cag Gln	atg Met	tac Tyr 35	ttc Phe	atg Met	ata Ile	tca Ser	ttg Leu 40	gga Gly	aac Asn	aca Thr	gac Asp	agt Ser 45	tat Tyr	ata Ile	cta Leu	145
gct Ala	gca Ala 50	atg Met	gca Ala	tat Tyr	gac Asp	cga Arg 55	gct Ala	gtg Val	gct Ala	atc Ile	agt Ser 60	cgc Arg	ccg Pro	ctt Leu	cat His	193
tat Tyr 65	gca Ala	aca Thr	att Ile	atg Met	agt Ser 70	cca Pro	caa Gln	ctt Leu	tgt Cys	gtc Val 75	ctg Leu	ctg Leu	gtt Val	gct Ala	80 GJA 333	241

Ser Tr	rp Va	l Ile	Ala 85	Asn	Ala	Asn	Ala	Leu 90	Pro	His	Thr	Leu	Leu 95	Thr	
gct ac Ala Ar	ga tt rg Le	g tcc u Ser 100	ttc Phe	tgt Cys	ggc Gly	aat Asn	aag Lys 105	gat Asp	gtg Val	gcc Ala	aac Asn	ttc Phe 110	tac Tyr	tgt Cys	337
gac at Asp Il	t ac le Th 11	r Pro	ttg Leu	ctc Leu	cag Gln	ctg Leu 120	tcc Ser	tgt Cys	tct Ser	gac Asp	atc Ile 125	cgc Arg	ttc Phe	aat Asn	385
gtg aa Val Ly 13	ag at ys Me 30	g atg t Met	tac Tyr	ctt Leu	999 Gly 135	gtg Val	Gly ggg	gtc Val	ttc Phe	tct Ser 140	gtg Val	cca Pro	ctg Leu	ctg Leu	433
tgc at Cys II 145	tc at le Il	c atc e Ile	tcc Ser	tat Tyr 150	gtc Val	cgg Arg	gtc Val	ttt Phe	tcc Ser 155	aca Thr	gtc Val	ttg Leu	cgg Arg	gtt Val 160	481
cca to Pro Se	ct ac er Th	c aag r Lys	ggc Gly 165	ttc Phe	ctg Leu	aag Lys	gcc Ala	ttg Leu 170	tcc Ser	acc Thr	tgt Cys	ggc Gly	tct Ser 175	cac His	529
ctg ac Leu Tl	ca gt hr Va	g gtg l Val 180	Ser	ttg Leu	tat Tyr	tat Tyr	ggg Gly 185	aca Thr	gtc Val	atg Met	ggc Gly	atg Met 190	tat Tyr	ttc Phe	577
cgg co Arg P	cc ct ro Le 19	u Thr	agt Ser	tac Tyr	agt Ser	ctg Leu 200	aag Lys	cat His	gca Ala	ttg Leu	ata Ile 205	act Thr	gtg Val	atg Met	625
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Asn H	lis Le	eu Let 20	ı Gly	Ser	Lys	Ala	Ile 25	Ser	Phe	Gly	Gly	Cys 30	Met	Ala	
Gln M	Met Ty 3!		e Met	: Ile	Ser	Leu 40	Gly	Asn	Thr	Asp	Ser 45	Tyr	Ile	. Leu	
Ala A 5	Ala Mo 50	et Ala	а Туг	: Asp	Arg 55	, Ala	ı Val	Ala	Ile	Ser 60	Arg	Pro	Leu	His	
Tyr A	Ala T	hr Ile	e Met	Ser	Pro	Glr	ı Leu	Cys	val	Leu	ı Lev	Val	Ala	Gly	

75

Ser Trp Val Ile Ala Asn Ala Asn Ala Leu Pro His Thr Leu Leu Thr 90

70

Ala Arg Leu Ser Phe Cys Gly Asn Lys Asp Val Ala Asn Phe Tyr Cys 105

Asp Ile Thr Pro Leu Leu Gln Leu Ser Cys Ser Asp Ile Arg Phe Asn 115 120

Val Lys Met Met Tyr Leu Gly Val Gly Val Phe Ser Val Pro Leu Leu 135

Cys Ile Ile Ile Ser Tyr Val Arg Val Phe Ser Thr Val Leu Arg Val 155

Pro Ser Thr Lys Gly Phe Leu Lys Ala Leu Ser Thr Cys Gly Ser His

Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly Met Tyr Phe

Arg Pro Leu Thr Ser Tyr Ser Leu Lys His Ala Leu Ile Thr Val Met 200

Tyr Thr Ala Val Thr Pro 210

<210> 386 <211> 649

<212> DNA

<213> Mus musculus domesticus

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<222> (1)..(649)

<223> Taxon = 10092; clone = OR15-71M24; Accession DDBJ/EMBL/GenBank = AF073967

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<222> (2)..(649)
<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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caa atg tat ttc ttt gtg gct ttt ggt att aca gac agt ttc ctt ttg 145

Gln Met Tyr 35	Phe Phe	Val Ala	Phe Gly	Ile 7	Thr Asp	Ser P 45	he Leu	Leu	
gct gcg ato Ala Ala Met 50	g gcc att : Ala Ile	gac cgc Asp Arg 55	tat gtt Tyr Val	gct a	att tgc Ile Cys 60	aat c Asn P	cg ctt ro Leu	cat His	193
tac aac aca Tyr Asn Thi 65				Cys 1					241
tcc tgg gca Ser Trp Ala	gtg tco Val Ser 85	cat ctt His Leu	cac tcc His Ser	ctc a Leu : 90	acc cac Thr His	aca a Thr I	tt ctc le Leu 95	atg Met	289
ggt cgc cto Gly Arg Leo	tct tto Ser Phe 100	tgt gga Cys Gly	ccc aat Pro Asn 105	Val :	att cat Ile His	His P	tc ttt he Phe 10	tgt Cys	337
gat gtc cag Asp Val Gli	n Pro Leu	gctg aca Leu Thr	ctc tcc Leu Ser 120	tgc ( Cys :	tct gac Ser Asp	acc t Thr S 125	ct atc Ser Ile	aat Asn	385
gag ctc ttg Glu Leu Lei 130	g gcc tto 1 Ala Phe	aca gag Thr Glu 135	Gly Ser	gtt g	gta atc Val Ile 140	atg a Met S	igc cct Ser Pro	ttt Phe	433
atc tta tte Ile Leu Le 145	g ttg tct 1 Leu Ser	ctt ata Leu Ile 150	tct ata Ser Ile	Phe '	act cgg Thr Arg 155	act g Thr V	gtt ctg /al Leu	agg Arg 160	481
gtc cct tc Val Pro Se	a ggg gaa r Gly Glu 165	ı Gly Arg	tac aaa Tyr Lys	gtt Val 170	ttc tct Phe Ser	acc t Thr C	gt ggg Cys Gly 175	Ser	529
cac ctc ac His Leu Th	a gtt gta r Val Val 180	a gca ctg L Ala Leu	ttc tat Phe Tyi 189	Gly	acc ata Thr Ile	Ile S	ca gtg Ser Val 190	tac Tyr	577
att cgc cc Ile Arg Pr 19	o Ser Se	e acc tac Thr Tyr	tca gto Ser Val 200	g aca L Thr	aag gac Lys Asp	cga ç Arg V 205	gtt gtc Val Val	act	625
gtc atc ta Val Ile Ty 210	t aca gta r Thr Vai	a gtt acc l Val Thr 215	Pro						649
<210> 387 <211> 216 <212> PRT <213> Mus	musculu	s domesti	cus				^		
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Leu Val As	p Ile Cy 5	s Phe Thi	Thr Va	l Ile 10	Val Pro	Gln I	Met Leu 15	ı Val	

Asn Leu Leu Thr Gln Arg Lys Thr Ile Leu Phe Ala Gln Cys Leu Thr

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Gln	Met	Tyr	Phe	Phe	Val	Ala	Phe	Gly	Ile	Thr	Asp	Ser	Phe	Leu	Leu
		35					40					45			

Ala Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu His

Tyr Asn Thr Val Met Ser Pro Arg Arg Cys Arg Leu Leu Val Val Ala

Ser Trp Ala Val Ser His Leu His Ser Leu Thr His Thr Ile Leu Met 85

Gly Arg Leu Ser Phe Cys Gly Pro Asn Val Ile His His Phe Phe Cys 105 100

Asp Val Gln Pro Leu Leu Thr Leu Ser Cys Ser Asp Thr Ser Ile Asn 120 125

Glu Leu Leu Ala Phe Thr Glu Gly Ser Val Val Ile Met Ser Pro Phe

Ile Leu Leu Ser Leu Ile Ser Ile Phe Thr Arg Thr Val Leu Arg 150

Val Pro Ser Gly Glu Gly Arg Tyr Lys Val Phe Ser Thr Cys Gly Ser 165

His Leu Thr Val Val Ala Leu Phe Tyr Gly Thr Ile Ile Ser Val Tyr 180

Ile Arg Pro Ser Ser Thr Tyr Ser Val Thr Lys Asp Arg Val Val Thr 205

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<213> Mus musculus domesticus

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<222> (1)..(649)

<223> Taxon = 10092; clone = OR18M; Accession DDBJ/EMBL/GenBank = AF073968

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<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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aac atg cag atc cag gac aca ccc ata tcc tat gtg gct tgt ctg aca Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu Thr 20 25 30	97
caa atg tac ttt ttc agt gtt ttt gga agt ctg gag ata ttc ctt ctt Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu 35 40 45	145
gta gtc ctg gcc tat gac cgc tat gtg gcc atc tgt tta ccc ctt caa Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln 50 55 60	193
tat tcc agc atc atg agc ccc aat ctc tgt gtg tgt gtg gtg ttc Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe 65 70 75 80	241
tgc tgg gta ttt att gtg ttt tat gcc atg ttt cac aca cta ctc ttg Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu 85 90 95	289
gct aga ttg tca ttt tgt aag aac aat gtg atc cca cac ttt ttc tgt Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys 100 105 110	337
gac ata tct gcc ctt ctg aag ttg gca tgc tct gat gtt tat att aat Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn 115 120	385
gaa tta atg ata ctt atc ttg gga ggg ttt ctt ctt gtc atc tca ctc Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu 130 135	433
tta ctc atc att gta tcc tat gta caa att gtc tcc tca att tta agg Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg 145 150 155 160	481
att tot tot act ogg got ato cat aag oto tto too acc tgt ggo toa Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser 165 170 175	529
cac ctg tct gtg gtc tca ctg ttc tat ggg aca att att ggt ctg tac His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190	577
tta tgt cca tca gct aat aac tct act gaa aag gag act gcc atg tcc Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser 195 200 205	625
ctg atg tac aca gtg gtg act ccc Leu Met Tyr Thr Val Val Thr Pro 210 215	649
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Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu 35 40 45

Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln 50 55 60

Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe 65 70 75 80

Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu Leu 85 90 95

Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Cys 100 105 110

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn 115 120 125

Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu 130 135 140

Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg 145 150 155 160

Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190

Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser 195 200 205

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caa Gln	aca Thr	tac Tyr 35	ttc Phe	ttt Phe	atg Met	gtt Val	ttt Phe 40	gga Gly	gat Asp	atg Met	gag Glu	agc Ser 45	ttc Phe	ctt Leu	ctt Leu	145
gtg Val	gcc Ala 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgc Arg 55	tat Tyr	gtg Val	gcc Ala	atc Ile	tgc Cys 60	ttc Phe	cct Pro	ctg Leu	cat His	193
tac Tyr 65	acc Thr	agc Ser	atc Ile	atg Met	agt Ser 70	ccc Pro	aaa Lys	ctc Leu	tgt Cys	ggt Gly 75	tgt Cys	cta Leu	atg Met	ctg Leu	cta Leu 80	241
ttg Leu	tgg Trp	atg Met	cta Leu	aca Thr 85	aca Thr	tcc Ser	cat His	gcc Ala	atg Met 90	atg Met	cat His	act Thr	ctc Leu	ctt Leu 95	gca Ala	289
gca Ala	aga Arg	ttg Leu	tct Ser 100	ttt Phe	tgt Cys	gag Glu	aac Asn	aat Asn 105	gțg Val	atc Ile	ctc Leu	aat Asn	ttt Phe 110	ttc Phe	tgt Cys	337
gac Asp	cta Leu	ttt Phe 115	gtt Val	ctc Leu	cta Leu	aag Lys	ctg Leu 120	gct Ala	tgc Cys	tca Ser	gac Asp	act Thr 125	tat Tyr	gtt Val	aat Asn	385
gag Glu	ttg Leu 130	atg Met	ata Ile	ttt Phe	ata Ile	atg Met 135	agt Ser	tcc Ser	ctc Leu	ctc Leu	att Ile 140	gtt Val	att Ile	cca Pro	ttt Phe	433
ttc Phe 145	ctc Leu	att Ile	gtc Val	atg Met	tct Ser 150	tat Tyr	gca Ala	agg Arg	atc Ile	att Ile 155	gcc Ala	tcc Ser	att Ile	ctt Leu	aag Lys 160	481
gtt Val	cca Pro	tct Ser	att Ile	caa Gln 165	Gly	atc Ile	tac Tyr	aag Lys	gtc Val 170	Phe	tcc Ser	acc Thr	tgt Cys	ggt Gly 175	tcc Ser	529
cat His	ctg Leu	tct Ser	gtg Val 180	Val	acc Thr	ttg Leu	ttt Phe	tat Tyr 185	Gly	aca Thr	att Ile	att Ile	ggt Gly 190	Leu	tac Tyr	577
tta Leu	tgt Cys	cca Pro	Ser	ggt Gly	aat Asn	aat Asn	tcc Ser 200	Thr	gta Val	aag Lys	ggg Gly	act Thr 205	gtc Val	atg Met	gcc Ala	625
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Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His

Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Gly Cys Leu Met Leu Leu 75

Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu Ala

Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Leu Asn Phe Phe Cys

Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn

Glu Leu Met Ile Phe Ile Met Ser Ser Leu Leu Ile Val Ile Pro Phe

Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ala Ser Ile Leu Lys 150 145

Val Pro Ser Ile Gln Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Ser 165

His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180

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## Met Met Tyr Thr Val Val Thr Pro 210 215

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caa Gln	gta Val	ttc Phe 35	ttt Phe	ttc Phe	ata Ile	cta Leu	ttt Phe 40	gga Gly	gtt Val	tta Leu	gat Asp	aac Asn 45	ttt Phe	ctt Leu	cta Leu	145	
gct Ala	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cga Arg 55	tat Tyr	gtg Val	gca Ala	atc Ile	tgt Cys 60	cac His	cct Pro	ctg Leu	cac His	193	
tat Tyr 65	atg Met	gtc Val	atc Ile	atg Met	aac Asn 70	cgc Arg	cgc Arg	ctc Leu	tgt Cys	gga Gly 75	ttt Phe	tta Leu	gtt Val	ttg Leu	80 GJA aaa	241	
tct Ser	tgg Trp	gtc Val	aca Thr	aca Thr 85	gca Ala	ttg Leu	aat Asn	tcc Ser	ttg Leu 90	ctg Leu	cag Gln	agt Ser	tca Ser	atg Met 95	gca Ala	289	
ctg Leu	cgg Arg	ctg Leu	tcc Ser 100	ttt Phe	tgt Cys	aca Thr	gac Asp	ttg Leu 105	aaa Lys	att Ile	ccc Pro	cac His	ttt Phe 110	gtt Val	tgt Cys	337	
gag Glu	ctt Leu	aat Asn 115	caa Gln	ctg Leu	gta Val	cta Leu	ctt Leu 120	gcc Ala	tgt Cys	aat Asn	gac Asp	acc Thr 125	ttt Phe	cct Pro	aat Asn	385	
gac Asp	atg Met 130	gtg Val	atg Met	tac Tyr	ttt Phe	gca Ala 135	gct Ala	ata Ile	ctg Leu	ctg Leu	ggt Gly 140	ggt Gly	ggt Gly	cct Pro	ctt Leu	433	
gct Ala 145	ggc Gly	atc Ile	ctt Leu	tac Tyr	tct Ser 150	tat Tyr	tct Ser	aag Lys	ata Ile	gtt Val 155	tcc Ser	tcc Ser	ata Ile	cgt Arg	gca Ala 160	481	
atc Ile	tca Ser	tca Ser	tca Ser	cag Gln 165	ggg ggg	aag Lys	tat Tyr	aaa Lys	gca Ala 170	Ser	tcc Ser	acc Thr	tgt Cys	gca Ala 175	tcc Ser	529	

cac ctc tca gtt gtt tca tta ttc tat tct aca ctc ttg ggt gcg tat His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Leu Leu Gly Ala Tyr 180 185 190	577
ctt agt tct tct ttt aca caa aac tca cac tca act gca cga gca tct Leu Ser Ser Ser Phe Thr Gln Asn Ser His Ser Thr Ala Arg Ala Ser 195 200 205	625
gtt atg tac agt gtg gtc acc ccc Val Met Tyr Ser Val Val Thr Pro 210 215	649
<210> 393 <211> 216 <212> PRT <213> Mus musculus domesticus	
<220> <221> misc_feature <222> (1)(649) <223> Taxon = 10092; clone = OR21M; Accession DDBJ/EMBL/GenBank	= AF073970
<400> 393	
Phe Ala Asp Ile Cys Phe Thr Ser Ala Ser Ile Pro Lys Met Leu Val 1 5 10 15	
Asn Ile Gln Thr Lys Asn Lys Val Ile Thr Tyr Glu Gly Cys Ile Ser 20 25 30	
Gln Val Phe Phe Phe Ile Leu Phe Gly Val Leu Asp Asn Phe Leu Leu 35 . 40 45	
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His 50 55 60	
Tyr Met Val Ile Met Asn Arg Arg Leu Cys Gly Phe Leu Val Leu Gly 65 70 75 80	
Ser Trp Val Thr Thr Ala Leu Asn Ser Leu Leu Gln Ser Ser Met Ala 85 90 95	
Leu Arg Leu Ser Phe Cys Thr Asp Leu Lys Ile Pro His Phe Val Cys 100 105 110	
Glu Leu Asn Gln Leu Val Leu Leu Ala Cys Asn Asp Thr Phe Pro Asn 115 120 125	
Asp Met Val Met Tyr Phe Ala Ala Ile Leu Leu Gly Gly Gly Pro Leu 130 135 140	
Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 145 150 155 160	
Ile Ser Ser Ser Gln Gly Lys Tyr Lys Ala Ser Ser Thr Cys Ala Ser	

His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Leu Leu Gly Ala Tyr
180 185 190

Leu Ser Ser Ser Phe Thr Gln Asn Ser His Ser Thr Ala Arg Ala Ser 195 200 205

Val Met Tyr Ser Val Val Thr Pro 210 215

<210> 394 <211> 649 <212> DNA <213> Mus musculus domesticus <220> <221> misc\_feature <222> (1)..(649)

<223> Taxon = 10092; clone = OR22M; Accession DDBJ/EMBL/GenBank = AF073971

<220> <221> CDS <222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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aac atg cag agc cag gac tca tcc atc acc tat gca gga tgc ctg aca

Asn Met Gln Ser Gln Asp Ser Ser Ile Thr Tyr Ala Gly Cys Leu Thr

20 25 30

caa atg tac ttt ttc ttg ctc ttt gga gac ctt gag agc ttc ctc ctt 145 Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu 35 40 45

gtg gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc ccc ctt cat
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
50 55 60

tac atg agc atc atg agc ccc agc ctc tgt gtg agt ctg gtg ctg ctg

Tyr Met Ser Ile Met Ser Pro Ser Leu Cys Val Ser Leu Val Leu

65 70 75 80

tcc tgg gtg ctg acc act ttc cat gcc atg ctg cat acc ctg ctc atg
Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
90
95

gcc aga ttg tca ttc tgt gag gac aat gtg atc ccc tac ttt ttc tgt
Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro Tyr Phe Phe Cys
100 105 110

gac atg tct gct ctg ctg aag ctg tcc tgc tct gac act cac gtt aat
Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn
115 120 125

gaa ttg gtg ata ttt gtc aca gga ggc ctg atc ctt gtc att cca ttt 433 Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Ile Pro Phe

130 135 140 gtg ctc atc ctt gtg tcc tat gca cga att gtg tcc tcc att ctc aag 481 Val Leu Ile Leu Val Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys gtc ccg tct gct cga ggc atc cgt aaa gcc ttc tcc acc tgt ggg tcc 529 Val Pro Ser Ala Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser 170 165 cac ctg tct gtg gtg tca ctg ttc tat ggg aca atc att ggt ctg tac His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 577 180 tta tgt cca tca gct gat aac tct act gtg aag gaa act gtc atg gcc Leu Cys Pro Ser Ala Asp Asn Ser Thr Val Lys Glu Thr Val Met Ala 625 200 195 649 atg atg tac aca gtg gtg act ccc Met Met Tyr Thr Val Val Thr Pro 215 <210> 395 <211> 216 <212> PRT <213> Mus musculus domesticus <220> <221> misc\_feature <222> (1)..(649) Taxon = 10092; clone = OR22M; Accession DDBJ/EMBL/GenBank = AF073971 <223> <400> 395 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln Asn Met Gln Ser Gln Asp Ser Ser Ile Thr Tyr Ala Gly Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Ser Leu Cys Val Ser Leu Val Leu Leu 70 Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met

Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro Tyr Phe Phe Cys

Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn 115 120 125

Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Ile Pro Phe 130 135 140
Val Leu Ile Leu Val Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys 145 150 155 160
Val Pro Ser Ala Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190
Leu Cys Pro Ser Ala Asp Asn Ser Thr Val Lys Glu Thr Val Met Ala 195 200 205
Met Met Tyr Thr Val Val Thr Pro 210 215
<210> 396 <211> 649 <212> DNA <213> Mus musculus domesticus
<220> <221> misc_feature <222> (1)(649) <223> Taxon = 10092; clone = OR25M; Accession DDBJ/EMBL/GenBank = AF073972
<220> <221> CDS <222> (2)(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7
<pre>&lt;400&gt; 396 c ttc act gac ctc tgc ttt tct act gtc aca atg ccc aat ttc ctg caa 49   Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln</pre>
aac atg cag agc caa gta tca tcc att ccc tat gca ggc tgc ctt gca 97 Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala 20 25 30
caa atg tac ttc ttt ttg ttt ttc ggt gat gtt gag agt tta ctc ctt 145 Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu Leu 35 40 45
gtt gcc atg gcc tat gac cgt tat gtg gcc atc tgc ttc cct ctt cat 193 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60
tat acc aga atc atg agc cca aac ctc tgt gtg agt atg gtg ctg ctg 241 Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu 65 70 75 80
289

act agg ttg tct ttc tgt aaa aac aat gtg atc ccc cat ttt ttc tgt  Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Cys  100  105  337													
gac ctt tct gct ctc ctg aag ctg gcc tgc tct gat att cac att aat Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 115 120 125													
gag tta atg ata att gga gca ctt gtt gtt ata ctt cca ttt Glu Leu Met Ile Met Ile Gly Ala Leu Val Val Ile Leu Pro Phe 130 135 140													
cta ctc atc ata gtg tct tat gcg cac att gtc tcc tcc att ctc aaa Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu Lys 145 150 155 160													
gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggg tct Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175													
cat ctg tct gtg gtg tca ctg ttc tat ggg tca gtc att gtt ctg tac  His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr  180 185 190													
tta tgt cca tca tct aat aac tct act gtg aag gat act gtc atg tct Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser 195 200 205													
atg atg tac act gtg gtg att ccc Met Met Tyr Thr Val Val Ile Pro 210 215													
<210> 397 <211> 216 <212> PRT <213> Mus musculus domesticus													
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<400> 397													
Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln 1 5 10 15													
Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala 20 25 30													
Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu Leu 35 40 45													
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His													
50 55 60													



Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys 105

90

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn

Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe

Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu Lys 150

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170

His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr 185

Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser 205

Met Met Tyr Thr Val Val Ile Pro

85

<210> 398

<211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc\_feature

(1)..(649) <222>

<223> Taxon = 10092; clone = OR27M; Accession DDBJ/EMBL/GenBank = AF073973

<220>

<221> CDS

<222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 398

c ttc act gac ctc tgc ttt tct act gtc aca atg ccc aat ttc ctg caa 49 Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln

aac atg cag agc caa gta tca tcc att ccc tat gca ggc tgc ctt gca 97 Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala

caa atg tac ttc ttt ttg ttt ttt ggt gat gtt gag agt tta ctc ctt 145 Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu

gtt gcc atg gcc tat gac cgt tat gtg gcc atc tgc tcc cct ctt cat Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu His

tat Tyr 65	acc Thr	aga Arg	atc Ile	atg Met	agc Ser 70	cca Pro	aac Asn	ctc Leu	tgt Cys	gtg Val 75	agt Ser	atg Met	gtg Val	ctg Leu	ctg Leu 80	241
tcc Ser	tgg Trp	gca Ala	ctg Leu	aca Thr 85	aca Thr	ttg Leu	tat Tyr	gcc Ala	atg Met 90	ttg Leu	cac His	act Thr	ttg Leu	ctc Leu 95	tta Leu	289
act Thr	agg Arg	ttg Leu	tct Ser 100	ttc Phe	tgt Cys	aaa Lys	aac Asn	aat Asn 105	gtg Val	atc Ile	ccc Pro	cat His	ttt Phe 110	ttc Phe	tgt Cys	337
gac Asp	ctt Leu	tct Ser 115	gct Ala	ctc Leu	ctg Leu	aag Lys	ctg Leu 120	gcc Ala	tgc Cys	tct Ser	gat Asp	att Ile 125	cac His	att Ile	aat Asn	385
gag Glu	tta Leu 130	atg Met	ata Ile	atg Met	ata Ile	att Ile 135	gga Gly	gca Ala	ctt Leu	gtt Val	gtt Val 140	ata Ile	ctt Leu	cca Pro	ttt Phe	433
cta Leu 145	ctc Leu	atc Ile	ata Ile	gtg Val	tct Ser 150	tat Tyr	gcg Ala	cac His	att Ile	gtc Val 155	tcc Ser	tcc Ser	act Thr	ctc Leu	aaa Lys 160	481
gtc Val	cct Pro	tca Ser	act Thr	cga Arg 165	ggc Gly	atc Ile	cac His	aag Lys	gtc Val 170	ttc Phe	tcc Ser	act Thr	tgt Cys	ggt Gly 175	tct Ser	529
cat His	ctg Leu	tct Ser	gtg Val 180	gtg Val	tca Ser	ctg Leu	ttc Phe	tat Tyr 185	Gly 999	tca Ser	gtc Val	att Ile	gtt Val 190	ctg Leu	tac Tyr	57 <b>7</b>
tta Leu	tgt Cys	cca Pro 195	tca Ser	tct Ser	aat Asn	aac Asn	tct Ser 200	act Thr	gtg Val	aag Lys	gat Asp	act Thr 205	Val	atg Met	tct Ser	625
atg Met	atg Met 210	tac Tyr	act Thr	gtg Val	gtg Val	act Thr 215	ccc Pro									649
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<210> 399 <211> 216

<212> PRT

<213> Mus musculus domesticus

<220>

<221> misc\_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR27M; Accession DDBJ/EMBL/GenBank = AF073973

Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln

Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu

- Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu His
- Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu
- Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu
- Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys
- Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
- Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe
- Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Thr Leu Lys 145
- Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165
- His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr 185 180
- Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser 200
- Met Met Tyr Thr Val Val Thr Pro
- <210> 400
- <211> 649
- <212> DNA
- <213> Mus musculus domesticus
- <220>
- <221> misc\_feature
- <222> (1)...(649)
- <223> Taxon = 10092; clone = OR28M; Accession DDBJ/EMBL/GenBank = AF073974
- <220>
- <221> CDS
- (2)..(649) <222>
- <223> Product = olfactory receptor; region between transmembrane domains
- <400> 400
- 49 a gtg gtg gac atc tgc tac acc tcc agt ggg gtc ccc cag atg ctg gca Val Val Asp Ile Cys Tyr Thr Ser Ser Gly Val Pro Gln Met Leu Ala 10

cac His	ttc Phe	ctc Leu	atg Met 20	gag Glu	aaa Lys	aag Lys	acc Thr	atc Ile 25	tct Ser	ttt Phe	gcc Ala	cta Leu	tgt Cys 30	Gly 999	acc Thr	97	
cag Gln	ctc Leu	ttc Phe 35	ttt Phe	gct Ala	ctg Leu	act Thr	ctt Leu 40	ggg Gly	gga Gly	act Thr	gag Glu	ttt Phe 45	ctg Leu	ttg Leu	ctg Leu	145	
act Thr	gcc Ala 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgc Arg 55	tat Tyr	gtg Val	gct Ala	gtc Val	tgt Cys 60	aat Asn	cca Pro	tta Leu	cgg Arg	193	
tac Tyr 65	aca Thr	gtg Val	gtg Val	atg Met	aac Asn 70	cca Pro	agg Arg	ctc Leu	tgc Cys	atg Met 75	ggt Gly	cta Leu	gca Ala	ggt Gly	gtc Val 80	241	
tct Ser	tgg Trp	ttt Phe	gtg Val	ggt Gly 85	gta Val	gtt Val	aat Asn	tct Ser	gct Ala 90	gtg Val	gag Glu	aca Thr	gca Ala	gtc Val 95	acc Thr	289	
atg Met	tac Tyr	ctt Leu	ccc Pro 100	acc Thr	tgt Cys	gly ggg	cac His	aat Asn 105	gta Val	ctc Leu	aac Asn	cat His	gtg Val 110	gcc Ala	tgt Cys	337	
gag Glu	aca Thr	ctg Leu 115	gca Ala	ctg Leu	gtc Val	aga Arg	ctg Leu 120	gcc Ala	tgt Cys	gtg Val	gac Asp	atc Ile 125	acc Thr	ctc Leu	aac Asn	385	
caa Gln	gtg Val 130	gtg Val	ata Ile	ctg Leu	gct Ala	tct Ser 135	agt Ser	gtg Val	gtg Val	gtg Val	ctg Leu 140	atg Met	ata Ile	ccc Pro	tgc Cys	433	
tct Ser 145	ctg Leu	gtc Val	tct Ser	ctg Leu	tcc Ser 150	tat Tyr	gcc Ala	cac His	att Ile	gta Val 155	gct Ala	gcc Ala	atc Ile	atg Met	aag Lys 160	481	
atc Ile	cgt Arg	tct Ser	acc Thr	cag Gln 165	gga Gly	cgc Arg	cgc Arg	aaa Lys	gcc Ala 170	ttt Phe	gag Glu	acc Thr	tgt Cys	gcc Ala 175	tcc Ser	529	
cat His	ctg Leu	act Thr	gtg Val 180	Val	tcc Ser	atg Met	tct Ser	tat Tyr 185	Gly	atg Met	gcc Ala	ctc Leu	ttc Phe 190	Thr	tac Tyr	577	
ctg Leu	Gln	cct Pro 195	Ala	Ser	aca Thr	Ala	Ser	Ala	gag Glu	cag Gln	gac Asp	aag Lys 205	Val	gta Val	gtg Val	625	
atc Ile	ttc Phe 210	Tyr	gct Ala	ttg Leu	gtc Val	acc Thr 215	ccc Pro									649	
<21 <21 <21 <21	1> 2>	401 216 PRT Mus	musc	ulus	dom	esti	cus										
<22 <22 <22 <22	1> 2>	(1)	. (64	ture 9) 1009		lone	= 0	R28M	I; Ac	cess	ion	DDBJ	/EME	sL/Ge	nBank	= AF0739	174
< 40	0>	401															
1/21	17 = 1	λαν	, T1=	Cve	. Tvr	Thr	Ser	Ser	- Glv	val	Pro	Gln	Met	. Leu	Ala		

Val Val Asp Ile Cys Tyr Thr Ser Ser Gly Val Pro Gln Met Leu Ala

His Phe Leu Met Glu Lys Lys Thr Ile Ser Phe Ala Leu Cys Gly Thr 20 25 30

Gln Leu Phe Phe Ala Leu Thr Leu Gly Gly Thr Glu Phe Leu Leu 40 45

Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Arg 50 55 60

Tyr Thr Val Val Met Asn Pro Arg Leu Cys Met Gly Leu Ala Gly Val
65 70 75 80

Ser Trp Phe Val Gly Val Val Asn Ser Ala Val Glu Thr Ala Val Thr 85 90 95

Met Tyr Leu Pro Thr Cys Gly His Asn Val Leu Asn His Val Ala Cys 100 105 110

Glu Thr Leu Ala Leu Val Arg Leu Ala Cys Val Asp Ile Thr Leu Asn 115 120 125

Gln Val Val Ile Leu Ala Ser Ser Val Val Val Leu Met Ile Pro Cys 130 135 140

Ser Leu Val Ser Leu Ser Tyr Ala His Ile Val Ala Ala Ile Met Lys 145 150 155 160

Ile Arg Ser Thr Gln Gly Arg Arg Lys Ala Phe Glu Thr Cys Ala Ser 165 170 175

His Leu Thr Val Val Ser Met Ser Tyr Gly Met Ala Leu Phe Thr Tyr 180 185 190

Leu Gln Pro Ala Ser Thr Ala Ser Ala Glu Gln Asp Lys Val Val Val 195 200 205

Ile Phe Tyr Ala Leu Val Thr Pro 210 215

<210> 402

<211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc\_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR29M; Accession DDBJ/EMBL/GenBank = AF073975

<220>

<221> CDS <222> (2)(649) <223> Product = olfactory receptor; region between transmembrane TM2 and TM7	domains													
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aaa ttt gtc atg gtg aag agt gtc att tct ttt gca gaa tgc atg gct Lys Phe Val Met Val Lys Ser Val Ile Ser Phe Ala Glu Cys Met Ala 20 25 30	97													
cag ttt tac tta ttt gat gtt ttt gct gtt tca gag tgt cac atg ctg Gln Phe Tyr Leu Phe Asp Val Phe Ala Val Ser Glu Cys His Met Leu 35 40 45	145													
gct gtc atg gct tat gat cgc tat gtt gcc atc tgt aac ccc ttg cta Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Leu 50 55 60	193													
tat aat gtt acc atg tct tac aaa gtg tgt tcc tgg atg gta gtg ggg Tyr Asn Val Thr Met Ser Tyr Lys Val Cys Ser Trp Met Val Val Gly 65 70 75 80	241													
gtg tat agt gta ggc ttg att tgt gcc aca ggg gaa aca gtc tgc ctg Val Tyr Ser Val Gly Leu Ile Cys Ala Thr Gly Glu Thr Val Cys Leu 85 90 95	289													
ctt aga ctg cta ttc tgc aaa gct gat gac ata aac cac tac ttc tgt Leu Arg Leu Leu Phe Cys Lys Ala Asp Asp Ile Asn His Tyr Phe Cys 100 105 110	337													
gat ctt tta cca cta ctg gaa caa tcc tgt tcc aat aca ttt atc aat Asp Leu Leu Pro Leu Leu Glu Gln Ser Cys Ser Asn Thr Phe Ile Asn 115 120 125	385													
gaa ata cta gga ctg tcc ttc agt tca ttt aat act act gtc cca gct Glu Ile Leu Gly Leu Ser Phe Ser Ser Phe Asn Thr Thr Val Pro Ala 130 135 140	433													
ctg acc atc ctc agt tcc tac atc ttc atc ata gcc agc atc ctc cgc Leu Thr Ile Leu Ser Ser Tyr Ile Phe Ile Ile Ala Ser Ile Leu Arg 145 150 155 160	481													
att cct tcc act gaa ggc agg tcc aaa gcc ttc agc acc tgc agc tcc Ile Pro Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser 165 170 175	529													
cac atc ttg gct gtt gct gtc ttc ttt ggg tct tta gca ttc atg tac His Ile Leu Ala Val Ala Val Phe Phe Gly Ser Leu Ala Phe Met Tyr 180 185 190	577													
ctt cag cca tca tca gtc agc tcc atg gac caa ggg aaa gtg tcc tct Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys Val Ser Ser 195 200 205	625													
gtg ttt tat acc att gtt gtg ccc Val Phe Tyr Thr Ile Val Val Pro 210 , 215	649													
<210> 403														

<sup>&</sup>lt;210> 403 <211> 216 <212> PRT

<213> Mus musculus domesticus

<220>

<221> misc\_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR29M; Accession DDBJ/EMBL/GenBank = AF073975

<400> 403

Phe Val Asp Leu Cys Gln Ser Ser Val Ile Met Pro Lys Met Leu Glu 1 10 15

Lys Phe Val Met Val Lys Ser Val Ile Ser Phe Ala Glu Cys Met Ala 20 25 30

Gln Phe Tyr Leu Phe Asp Val Phe Ala Val Ser Glu Cys His Met Leu 35 40 45

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Leu 50 55 60

Tyr Asn Val Thr Met Ser Tyr Lys Val Cys Ser Trp Met Val Val Gly 65 70 75 80

Val Tyr Ser Val Gly Leu Ile Cys Ala Thr Gly Glu Thr Val Cys Leu 85 90 95

Leu Arg Leu Leu Phe Cys Lys Ala Asp Asp Ile Asn His Tyr Phe Cys 100 105 110

Asp Leu Leu Pro Leu Leu Glu Gln Ser Cys Ser Asn Thr Phe Ile Asn 115 120 125

Glu Ile Leu Gly Leu Ser Phe Ser Ser Phe Asn Thr Thr Val Pro Ala 130 135 140

Leu Thr Ile Leu Ser Ser Tyr Ile Phe Ile Ile Ala Ser Ile Leu Arg 145 150 155 160

Ile Pro Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser 165 170 175

His Ile Leu Ala Val Ala Val Phe Phe Gly Ser Leu Ala Phe Met Tyr 180 185 190

Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys Val Ser Ser 195 200 205

Val Phe Tyr Thr Ile Val Val Pro 210 215

<210> 404

<211> 649 <212> DNA <213> Mus musculus domesticus												
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<220> <221> CDS <222> (2)(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7												
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aac atg cag agc caa gtt cct tca atc ccc tat gca ggc tgc ctg aca Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr 20 25 30	97											
caa atg tac ttc ttt ttg ttt ttt gga gat ctt gag agc ttc ctc ctt Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu 35 40 45	145											
gtg gcc atg gcc tat gac cga tat gta gcc atc tgc ttc cct ctt cat Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60	193											
tac acc agc att atg agc ccc agg ctc tgt gtg agt ctt gtg ctg Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu 65 70 75 80	241											
tcc tgg ttg ctg acc atg tcc cat tcc atg ctg cac act ttg ctc tta Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu 85 90 95	289											
act agg ttg tct ttc tgt gaa aac aat gtg atc ccc cat ttt ttc tgt Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys 100 105 110	337											
gat ctg tct gct ctg ctg aag ctg gcc tgc tct gat att cac att aat Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 115 120 125	385											
gaa ttg gtg ata ttg atc ata gga ggg ctt gtt gtt ata ctt cca ttt Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe 130 135 140	433											
cta ctc gtc aca gtg tct tat gca cgc atc atc tcc tcc att ctc aag Leu Leu Val Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys 145 150 155 160	481											
gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggt tct Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175	529											
cac ctg tct gtg gtg tca ctg ttc tat ggg aca att att ggc ctc tac His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190	577											
tta tgt cca tct gct aat aac tct act cta aag gac act gtc atg tct Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser	625											

195 200 205

ctg atg tac act gtg gta act ccc Leu Met Tyr Thr Val Val Thr Pro 649

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<212> PRT

<213> Mus musculus domesticus

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<221> misc\_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR2M; Accession DDBJ/EMBL/GenBank = AF073976

<400> 405

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Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr 20 25 30

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu 35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 60

Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu 65 70 75 80

Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu 85 90 95

Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Cys 100 105 110

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 115 120 125

Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe 130 135 140

Leu Leu Val Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys 145 150 155 160

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190

## Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser 195 200 205

Leu Met Tyr Thr Val Val Thr Pro 210 215

<210><211><211><212><213>	406 650 DNA Mus m	nuscu	lus	dome	stic	us									
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cag aa Gln As	ac atg sn Met	cag Gln	atc Ile 20	cag Gln	gac Asp	aca Thr	ccc Pro	ata Ile 25	tcc Ser	tat Tyr	gtg Val	gct Ala	tgt Cys 30	ctg Leu	95
aca ca Thr Gl	aa atg ln Met	tac Tyr 35	ttt Phe	ttc Phe	agt Ser	gtt Val	ttt Phe 40	gga Gly	agt Ser	ctg Leu	gag Glu	ata Ile 45	ttc Phe	ctt Leu	143
ctt gt Leu Va	a gtc al Val 50	ctg Leu	gcc Ala	tat Tyr	gac Asp	cgc Arg 55	tat Tyr	gtg Val	gcc Ala	atc Ile	tgt Cys 60	tta Leu	ccc Pro	ctt Leu	191
caa ta Gln Ty	at tcc yr Ser	agc Ser	atc Ile	atg Met	agc Ser 70	ccc Pro	aat Asn	ctc Leu	tgt Cys	gtg Val 75	tgt Cys	gtg Val	gtg Val	gtg Val	239
ttc to Phe Cy 80	gc tgg ys Trp	gta Val	ttt Phe	att Ile 85	gtg Val	ttt Phe	tat Tyr	gcc Ala	atg Met 90	ttt Phe	cac His	aca Thr	cta Leu	ctc Leu 95	287
ttg go Leu Al	ct aga la Arg	ttg Leu	tca Ser 100	ttt Phe	tgt Cys	aag Lys	aac Asn	aat Asn 105	gtg Val	atc Ile	cca Pro	cac His	ttt Phe 110	ttc Phe	335
tgt ga Cys As	ac ata sp Ile	tct Ser 115	gcc Ala	ctt Leu	ctg Leu	aag Lys	ttg Leu 120	gca Ala	tgc Cys	tct Ser	gat Asp	gtt Val 125	tat Tyr	att Ile	383
aat g Asn G	aa tta lu Leu 130	Met	ata Ile	ctt Leu	atc Ile	ttg Leu 135	gga Gly	Gly aaa	ttt Phe	ctt Leu	ctt Leu 140	gtc Val	acc Thr	tca Ser	431
Leu L	ta ctc eu Leu 45	atc Ile	att Ile	gta Val	tcc Ser 150	Tyr	gta Val	caa Gln	att Ile	gtc Val 155	tcc Ser	tca Ser	att Ile	tta Leu	479

agg Arg 160	att Ile	tct Ser	tct Ser	act Thr	cgg Arg 165	gct Ala	atc Ile	cat His	aag Lys	ctc Leu 170	ttc Phe	tcc Ser	acc Thr	tgt Cys	ggc Gly 175	527
tca Ser	cac His	ctg Leu	tct Ser	gtg Val 180	gtc Val	tca Ser	ctg Leu	ttc Phe	tat Tyr 185	G1 y 999	gca Ala	att Ile	att Ile	ggt Gly 190	ctg Leu	575
tac Tyr	tta Leu	tgt Cys	cca Pro 195	tca Ser	gct Ala	aat Asn	aac Asn	tct Ser 200	act Thr	gaa Glu	aag Lys	gag Glu	act Thr 205	gcc Ala	atg Met	623
tcc Ser	ctg Leu	atg Met 210	tac Tyr	aca Thr	gtg Val	gtg Val	act Thr 215	ccc Pro								650
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Asn	Met	Gln	Ile 20	Gln	Asp	Thr	Pro	Ile 25	Ser	Tyr	Val	Ala	Cys 30	Leu	Thr	
Gln	Met	Tyr 35	Phe	Phe	Ser	Val	Phe 40	Gly	Ser	Leu	Glu	Ile 45	Phe	Leu	Leu	
Val	Val 50	Leu	Ala	Tyr	Asp	Arg 55	Tyr	Val	Ala	Ile	Cys 60	Leu	Pro	Leu	Gln	
Tyr 65	Ser	Ser	Ile	Met	Ser 70	Pro	Asn	Leu	Cys	Val 75	Cys	Val	Val	Val	Phe 80	
Cys	Trp	Val	Phe	Ile 85	· Val	Phe	Tyr	Ala	Met 90	Phe	His	Thr	Leu	. Leu 95	. Leu	
Ala	Arg	Leu	Ser		. Cys	Lys	Asn	Asn 105		Ile	Pro	His	Phe 110	Phe	e Cys	
Asp	Ile	Ser		Leu	ı Lev	ı Lys	120		a Cys	Ser	Asp	Val 125	Туг	: Ile	e Asn	
Glu	Leu 130		: Ile	Leu	ı Ile	e Leu 135		, Glλ	/ Phe	e Leu	140	ı Val	l Thi	: Sei	. Leu	
Leu	ı Leı	ı Ile	e Ile	· Val	L Sei	туг	· Val	Glr	n Ile	val	Ser	: Sei	c Ile	e Lei	ı Arg	

Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser 170

His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Ile Ile Gly Leu Tyr 185

Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser 200

Leu Met Tyr Thr Val Val Thr Pro 215 210

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<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc\_feature

(1)..(648) <222>

<223> Taxon = 10092; clone = OR4M; Accession DDBJ/EMBL/GenBank = AF073978

<220>

<221> CDS

<222> (2)..(646)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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aac atg cag atc cag gac aca ccc ata tcc tat gtg gct tgt ctg aca 97 Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu Thr 25

caa atg tac ttt ttc agt gtt ttt ggg agt ctg gag ata ttc ctt ctt 145 Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu 45 40

gta gtc ctg gcc tat gac cgc tat gtg gcc atc tgt tta ccc ctt caa 193 Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln

tat too ago ato atg ago coo aat oto tgt gtg tgt gtg gtg gtg tto 241 Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe 65 70

tgc tgg gta ttt att gtg ttt tat gcc atg ttt cac aca cta ctc ttg 289 Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu Leu

gct aga ttg tca ttt tgt aag aac aat gtg atc cca cac ttt ttc tgt 337 Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys 110 105

gac ata tct gcc ctt ctg aag ttg gca tgc tct gat gtt tat att aat Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn 385 115 120 125

	115				120					125				
gaa tta Glu Leu 130	atg at Met Il	a ctt e Leu	Ile	ttg Leu 135	gga Gly	Gly 333	ttt Phe	ctt Leu	ctt Leu 140	gtc Val	atc Ile	tca Ser	ctc Leu	433
tta ctc Leu Leu 145	atc at Ile Il	t gta e Val	tcc Ser 150	tat Tyr	gta Val	caa Gln	att Ile	gtc Val 155	tcc Ser	tca Ser	att Ile	tta Leu	agg Arg 160	481
att tct Ile Ser	tct ac Ser Th	ct cgg nr Arg 165	gct Ala	atc Ile	cat His	aag Lys	ctc Leu 170	ttc Phe	tcc Ser	acc Thr	tgt Cys	ggc Gly 175	tca Ser	529
cac ctg His Leu	Ser Va	g gtc al Val 80	tca Ser	ctg Leu	ttc Phe	tat Tyr 185	Gly 999	aca Thr	att Ile	att Ile	ggt Gly 190	ctg Leu	tac Tyr	577
tta tgt Leu Cys	cca to Pro Se 195	ca gct er Ala	aat Asn	aac Asn	tct Ser 200	act Thr	gaa Glu	aag Lys	gag Glu	act Thr 205	gcc Ala	atg Met	tcc Ser	625
ctg atg Leu Met 210	tac ao Tyr Tl	ca gtg nr Val	gtg Val	act Thr 215	cc									648
<211> 2 <212> F	09 15 RT lus mu	sculus	dome	esti	cus									
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<400> 4	09													
Phe Ser 1	Asp L	eu Cys 5	Phe	Ser	Ser	Val	Thr 10	Met	Pro	Lys	Leu	Leu 15	Gln	
Asn Met		le Gln O	Asp	Thr	Pro	Ile 25	Ser	Tyr	Val	Ala	Cys 30	Leu	Thr	
Gln Met	Tyr P 35	he Phe	. Ser	Val	Phe 40	Gly	Ser	Leu	Glu	Ile 45	Phe	Leu	Leu	
Val Val 50	Leu A	la Tyr	Asp	Arg 55	Tyr	Val	Ala	Ile	Cys 60	Leu	Pro	Leu	Gln	
Tyr Ser 65	Ser I	le Met	Ser 70	Pro	Asn	Leu	Cys	Val 75	Cys	Val	. Val	Val	Phe 80	
Cys Trp	Val F	he Ile 85	e Val	Phe	Tyr	Ala	Met 90	Phe	His	Thr	Leu	Leu 95	Leu	

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn 115 120 125
Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu 130 135 140
Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg 145 150 155 160
Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser 165 170 175
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190
Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser 195 200 205
Leu Met Tyr Thr Val Val Thr 210 215
<210> 410 <211> 649 <212> DNA <213> Mus musculus domesticus
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<220> <221> CDS <222> (2)(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7
<pre>&lt;400&gt; 410 c ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aag ttg ctg cag   Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln   1 5 10 15</pre>
aac atg cag agc cag gac cca tcc atc ccc tat gcc agc tgt ctg aca 97 Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Ser Cys Leu Thr 20 25 30
caa atg tac ttt ttc atg gct ttt ggg aac atg gaa att tat ctt ctt 145 Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Met Glu Ile Tyr Leu Leu 35 40 45
gtg gtc atg gcc tat gac cgc tat gtg gcc atc tgc ttc cct ctt cat  Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His  50  55  60
tac acc agc atc atg agc cct aag ctc tgt gtg tct ctg gtg gtt ctc Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu Val Val Leu 65 70 75 80

tct tgg gta ttt acc att ctg tat tcc atg tta cac acc cta ctc ttg Ser Trp Val Phe Thr Ile Leu Tyr Ser Met Leu His Thr Leu Leu 85 90 95	289												
gca aga ttg tca ttc tgt gag gac aat gtg atc ccc cac ttt ttc tgt Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys 100 105 110	337												
gac ata tct gcc ctg ctc aag ttg gcc tgc tct gac att tct att aat Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile Ser Ile Asn 115 120 125	385												
gaa cta atg ata ttt atc gtg gga ggg ctt gat act gta atc cca ttt Glu Leu Met Ile Phe Ile Val Gly Gly Leu Asp Thr Val Ile Pro Phe 130 135 140	433												
tta ctc att gtt gtt tcc tat gta caa att gtc tgc tcc att cta aag Leu Leu Ile Val Val Ser Tyr Val Gln Ile Val Cys Ser Ile Leu Lys 145 150 155 160	481												
ttc tca tct aca cgg ggc ata cac aag gtc ttc tcc acc tgt ggc tcc Phe Ser Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175	529												
cac ctg tct gtg gtc tca ctg ttc tat ggg aca att att ggt gtc tac His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Val Tyr 180 185 190	577												
ata tgc cca tca gct aat aac tct act gtg aag gag act gtc atg tcc Ile Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr Val Met Ser 195 200 205	625												
ctg atg tac aca gtg gtg acg ccc Leu Met Tyr Thr Val Val Thr Pro 210 215	649												
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Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln 1 5 10 15													
Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Ser Cys Leu Thr 20 25 30													
Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Met Glu Ile Tyr Leu Leu 35 40 45													
Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60 `													
Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu Val Val Leu													

Ser Trp Val Phe Thr Ile Leu Tyr Ser Met Leu His Thr Leu Leu Leu

70

Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys 105

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile Ser Ile Asn

Glu Leu Met Ile Phe Ile Val Gly Gly Leu Asp Thr Val Ile Pro Phe 130

Leu Leu Ile Val Val Ser Tyr Val Gln Ile Val Cys Ser Ile Leu Lys 150 145

Phe Ser Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 170

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Val Tyr

Ile Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr Val Met Ser 205

Leu Met Tyr Thr Val Val Thr Pro 210

<210> 412

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR6M; Accession DDBJ/EMBL/GenBank = AF073980

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<221> CDS

<222> (2)..(649)
<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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aac atg cag agc caa gtt cct tca atc ccc tat gca ggc tgc ctg aca 97 Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr 25

caa atg tac ttc ttt ttg ttt ttt gga gat ctt gag agc ttc ctc ctt 145 Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu

35 40 45

gtg Val	gcc Ala 50	atg Met	gcc Ala	tat Tyr	gac Asp	cga Arg 55	tat Tyr	gta Val	gcc Ala	atc Ile	tgc Cys 60	ttc Phe	cct Pro	ctt Leu	cat His	193
tac Tyr 65	acc Thr	agc Ser	att Ile	atg Met	agc Ser 70	ccc Pro	agg Arg	ctc Leu	tgt Cys	gtg Val 75	agt Ser	ctt Leu	gtg Val	ctg Leu	ctg Leu 80	241
tcc Ser	tgg Trp	ttg Leu	ctg Leu	acc Thr 85	atg Met	tcc Ser	cat His	tcc Ser	atg Met 90	ctg Leu	cac His	act Thr	ttg Leu	ctc Leu 95	tta Leu	289
act Thr	agg Arg	ttg Leu	tct Ser 100	ttc Phe	tgt Cys	gaa Glu	aac Asn	aat Asn 105	gtg Val	atc Ile	ccc Pro	cat His	ttt Phe 110	ttc Phe	tgt Cys	337
gat Asp	ctg Leu	tct Ser 115	gct Ala	ctg Leu	ctg Leu	aag Lys	ctg Leu 120	gcc Ala	tgc Cys	tct Ser	gat Asp	att Ile 125	cac His	att Ile	aat Asn	385
gaa Glu	ttg Leu 130	gtg Val	ata Ile	ttg Leu	atc Ile	ata Ile 135	gga Gly	Gly 999	ctt Leu	gtt Val	gtt Val 140	ata Ile	ctt Leu	cca Pro	ttt Phe	433
cta Leu 145	ctc Leu	gtc Val	aca Thr	gtg Val	cct Pro 150	tat Tyr	gca Ala	cgc Arg	atc Ile	atc Ile 155	tcc Ser	tcc Ser	att Ile	ctc Leu	aag Lys 160	481
gto Val	cct Pro	tca Ser	act Thr	cga Arg 165	ggc Gly	atc Ile	cac His	aag Lys	gtc Val 170	ttc Phe	tcc Ser	act Thr	tgt Cys	ggt Gly 175	tct Ser	529
cac His	ctg Leu	tct Ser	gtg Val 180	Val	tca Ser	ctg Leu	ttc Phe	tat Tyr 185	Gly	aca Thr	att Ile	att Ile	ggc Gly 190	ctc Leu	tac Tyr	577
tta Lev	tgt Cys	cca Pro	Ser	gct Ala	aat Asn	aac Asn	tct Ser 200	Thr	cta Leu	aag Lys	gac Asp	act Thr 205	vaı	atg Met	tct Ser	625
cto Lei	atg Met 210	Tyr	act Thr	gtg Val	gta Val	act Thr 215	Pro									649
<23 <23		413 216 PRT Mus	musc	ulus	don	esti	cus									
<22 <22		(1)	c_fea .(64 on =	9)		:lone	: = C	)R6M;	Acc	essi:	on E	DBJ/	'EMBL	ı/Gen	Bank	= AF073980
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Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr 20 25 30

- Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu
- Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 55
- Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu 75
- Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu
- Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys 105 100
- Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
- Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe 130
- Leu Leu Val Thr Val Pro Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys 150
- Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170
- His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180
- Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser 205
- Leu Met Tyr Thr Val Val Thr Pro 210
- <210> 414
- <211> 649
- <212> DNA
- <213> Mus musculus domesticus
- <220>
- <221> misc\_feature
- <222> (1)..(649)
- <223> Taxon = 10092; clone = OR7M; Accession DDBJ/EMBL/GenBank = AF073981
- <220>
- <221> CDS
- <222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7
- <400> 414

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aac ato Asn Med	g cag Gln	agc Ser 20	caa Gln	gta Val	tca Ser	tcc Ser	att Ile 25	ccc Pro	tat Tyr	gca Ala	ggc Gly	tgc Cys 30	ctt Leu	gca Ala	9	7
caa ato Gln Me	g tac Tyr 35	ttc Phe	ttt Phe	ttg Leu	ttt Phe	ttt Phe 40	ggt Gly	gat Asp	gtt Val	gag Glu	agc Ser 45	tta Leu	ctc Leu	ctt Leu	14	5
gtt gce Val Ala 50	c atg a Met	gcc Ala	tat Tyr	gac Asp	cgt Arg 55	tat Tyr	gtg Val	gcc Ala	atc Ile	tgc Cys 60	ttc Phe	cct Pro	ctt Leu	cat His	19	3
tat acc Tyr Th	c aga r Arg	atc Ile	atg Met	agc Ser 70	cca Pro	aac Asn	ctc Leu	tgt Cys	gtg Val 75	agt Ser	atg Met	gtg Val	ctg Leu	ctg Leu 80	24	1
tcc tg Ser Tr	g gca p Ala	ctg Leu	aca Thr 85	aca Thr	ttg Leu	tat Tyr	gcc Ala	atg Met 90	ttg Leu	cac His	act Thr	ttg Leu	ctc Leu 95	tta Leu	28	9
act ag Thr Ar	g ttg g Leu	tct Ser 100	ttc Phe	tgt Cys	aaa Lys	aac Asn	aat Asn 105	gtg Val	atc Ile	ccc Pro	cat His	ttt Phe 110	ttc Phe	tgt Cys	33	7
gac ct Asp Le	t tct u Ser 115	Ala	ctc Leu	ctg Leu	aag Lys	ctg Leu 120	gcc Ala	tgc Cys	tct Ser	gat Asp	att Ile 125	cac His	att Ile	aat Asn	38	15
gag tt Glu Le 13	u Met	ata Ile	atg Met	ata Ile	att Ile 135	gga Gly	gca Ala	ctt Leu	gtt Val	gtt Val 140	ata Ile	ctt Leu	cca Pro	ttt Phe	43	33
cta ct Leu Le 145	c atc u Ile	ata Ile	gtg Val	tct Ser 150	tat Tyr	gcg Ala	cac His	att Ile	gtc Val 155	tcc Ser	tcc Ser	att Ile	ctc Leu	aaa Lys 160	4.8	31
gtc cc Val Pr	t tca o Ser	act Thr	cga Arg 165	ggc Gly	atc Ile	cac His	aag Lys	gtc Val 170	ttc Phe	tcc Ser	act Thr	tgt Cys	ggt Gly 175	tct Ser	52	29
cat ct His Le	g tct u Ser	gcg Ala 180	Val	tca Ser	ctg Leu	ttc Phe	tat Tyr 185	61 y 999	tca Ser	gtc Val	att Ile	gtt Val 190	ctg Leu	tac Tyr	57	77
tta tg Leu Cy	t cca s Pro 195	Ser	tct Ser	aat Asn	aac Asn	tct Ser 200	act Thr	gtg Val	aag Lys	gat Asp	act Thr 205	vaı	atg Met	tct Ser	62	25
atg at Met Me 21	t Tyr	act Thr	gtg Val	gtg Val	act Thr 215	ccc Pro									64	49
<210><211><211><212><213>	216 PRT	musc	ulus	dom	ıesti	cus										
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Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln

Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 55

Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu 75

Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu

Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn

Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe 130

Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu Lys 145

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165

. His Leu Ser Ala Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr

Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser 200

Met Met Tyr Thr Val Val Thr Pro 210

<210> 416

<211> 649

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aat ata cag age cag gac cca tcc atc ccc tat gca gge tge ctg gca Asn Ile Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala 20 25 30	97
caa aca tac ttc ttt atg gtt ttt gga gat atg gag agc ttc ctt ctt Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu 35 40 45	145
gtg gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc cct ctg cat Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60	193
tac acc agc atc atg agt ccc aaa ctc tgt ggt tgt cta atg ctg cta Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Gly Cys Leu Met Leu Leu 65 70 75 80	241
ttg tgg atg cta aca aca tcc cat gcc atg atg cat act ctc ctt gca Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu Ala 85 90 95	289
gca aga ttg tct ttt tgt gag aac aat gtg atc ctc aat ttt ttc tgt Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Leu Asn Phe Phe Cys 100 105 110	337
gac cta ttt gta ctc cta aag ctg gct tgc tca gac act tat gtt aat Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn 115 120 125	385
gag ttg atg ata ttt ata atg agt tcc ctc ctc att gtt att cca ttt Glu Leu Met Ile Phe Ile Met Ser Ser Leu Leu Ile Val Ile Pro Phe 130 135 140	433
ttc ctc att gtc atg tct tat gca agg atc att gcc tcc att ctt aag Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ala Ser Ile Leu Lys 145 150 155 160	481
gtt cca tct att caa ggg atc tac aag gtc ttc tcc acc tgt ggt tcc Val Pro Ser Ile Gln Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Ser 165 170 175	529
cat ctg tct gtg gtg acc ttg ttt tat ggg aca att att ggt ctc tac His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190	577
tta tgt cca tca ggt aat aat tcc aca gta aag ggg act gtc atg gcc Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Gly Thr Val Met Ala 195 200 205	625
atg atg tac aca gcg gtg act ccc Met Met Tyr Thr Ala Val Thr Pro 210 215	649

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<210> 417
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<223> Taxon = 10092; clone = OR8M; Accession DDBJ/EMBL/GenBank = AF073982
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Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Gln 1 10 15

Asn Ile Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala 20 25 30

Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu 35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 60

Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Gly Cys Leu Met Leu Leu 65 70 75 80

Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu Ala 85 90 95

Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Leu Asn Phe Phe Cys 100 105 110

Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn 115 120 125

Glu Leu Met Ile Phe Ile Met Ser Ser Leu Leu Ile Val Ile Pro Phe 130 135 140

Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ala Ser Ile Leu Lys 145 150 155 160

Val Pro Ser Ile Gln Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190

Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Gly Thr Val Met Ala 195 200 205

Met Met Tyr Thr Ala Val Thr Pro

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AF073983
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<221> CDS
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                                                                             49
  Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
                                                                             97
aat ata cag act caa agc aag gcc att aca tat gca gac tgt att agc
Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala Asp Cys Ile Ser
cag atg tct gtc ttc ttg gtt ttt gca gaa ttg gac aac ttt ctc ctg
Gln Met Ser Val Phe Leu Val Phe Ala Glu Leu Asp Asn Phe Leu Leu
                                                                            145
gct gtg atg gcc tat gac cga tat gtg gct atc tgt cac cca tta tat
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr
                                                                            193
tac aca gtc att gtt aac caa cat ctc tgt ata ctg atg gtt ctg ctg
                                                                            241
Tyr Thr Val Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu
                      70
tee tgg gtt gtt age ate eta cat gee tte tta cag age tea att gtg
                                                                            289
Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val
                                        90
                                                                            337
cta cag ttg acc ttt tgt gga gat gta aaa att ccc cac ttc ttc tgt
Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro His Phe Phe Cys
                                   105
             100
                                                                            385
gag ctt aac cag ctg tct caa ctc aca tgt tca gac agc ttt tca agc
Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp Ser Phe Ser Ser
                                                     125
caa ctc ata atg aat ctt gta cct gtt cta ttg gca gtc att tcc ttc
                                                                            433
Gln Leu Ile Met Asn Leu Val Pro Val Leu Leu Ala Val Ile Ser Phe
                           135
agt agt atc ctt tac tct tat ttc aag ata gtg tcc tcc ata tgt tct
                                                                            481
Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser
                      150
atc tcc tca gtt caa ggg aag tac aag gca ttt tct aca tgt gtc tct
                                                                            529
Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser
                                        170
cac ctt tcc att gtc tcc tta ttt tat agt aca ggc ctt gga gtg tat
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His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr
                                185
gtc agt tot gtt gtg atc caa agc tot cac tot gct gca aga gcc tot
                                                                      625
Val Ser Ser Val Val Ile Gln Ser Ser His Ser Ala Ala Arg Ala Ser
                                                 205
                            200
                                                                       649
gtg atg tat act gtg gtc acc ccg
Val Met Tyr Thr Val Val Thr Pro
    210
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<212> PRT
<213> Mus musculus domesticus
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AF073983
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Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala Asp Cys Ile Ser
                                 25
            20
Gln Met Ser Val Phe Leu Val Phe Ala Glu Leu Asp Asn Phe Leu Leu
                             40
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr
Tyr Thr Val Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu
Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val
Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro His Phe Phe Cys
                                 105
Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp Ser Phe Ser Ser
         115
                             120
 Gln Leu Ile Met Asn Leu Val Pro Val Leu Leu Ala Val Ile Ser Phe
     130
 Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser
                     150
 145
```

Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser

His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr

Val Ser Ser Val Val Ile Gln Ser Ser His Ser Ala Ala Arg Ala Ser

Val Met Tyr Thr Val Val Thr Pro

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<211> 646

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<221> misc\_feature

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<221> CDS

<222> (2)..(646) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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att cac ata cta aga aat caa gcc att tcg ttc tct ggg tgc ctc aca 97 Ile His Ile Leu Arg Asn Gln Ala Ile Ser Phe Ser Gly Cys Leu Thr 25

145 cag ctg tat ttt ctc tgt gtg ttt gct gac atg gac aat ttc ctg ctg Gln Leu Tyr Phe Leu Cys Val Phe Ala Asp Met Asp Asn Phe Leu Leu 35

193 gct gtg atg gcc tat gac cga ttt gtg gcc ata tgc cac cct tta cac Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55

241 tac aca aca aag atg acc cat cag ctt tgt gcc ttt ctt gtt ggg Tyr Thr Thr Lys Met Thr His Gln Leu Cys Ala Phe Leu Val Val Gly 70

tcc tgg atg gta gcc agt ctg aat gct ctg ttg cac aca ctg ctc gtg 289 Ser Trp Met Val Ala Ser Leu Asn Ala Leu Leu His Thr Leu Leu Val 90

gct caa ctc tac ttc tgt ggg gac aat gtg atc ccc cac ttc ttc tgt 337 Ala Gln Leu Tyr Phe Cys Gly Asp Asn Val Ile Pro His Phe Phe Cys

gaa gtg act ccc ctg ctg aaa ctc tct tgc tca gac aca cat ctc aat 385 Glu Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn 115

gag ttg atg att ctt gct gtt gca ggg ctg ata atg tta gct cca ttt 433

Glu	Leu 130	Met	Ile	Leu	Ala	Val 135	Ala	Gly	Leu	Ile	Met 140	Leu	Ala	Pro	Phe	
gtt Val 145	tgc Cys	atc Ile	ctc Leu	ttg Leu	tct Ser 150	tat Tyr	atc Ile	ctt Leu	att Ile	gct Ala 155	tgt Cys	gcc Ala	atc Ile	ctg Leu	aaa Lys 160	481
atc Ile	tca Ser	tcc Ser	aca Thr	gga Gly 165	aga Arg	tgg Trp	aaa Lys	gcc Ala	ttc Phe 170	tct Ser	acc Thr	tgt Cys	ggc Gly	tca Ser 175	cac His	529
ttg Leu	gct Ala	gtt Val	gtg Val 180	tgc Cys	ctc Leu	ttc Phe	tat Tyr	ggc Gly 185	act Thr	atc Ile	ata Ile	tcc Ser	ctg Leu 190	tat Tyr	ttc Phe	577
aac Asn	ccc Pro	tca Ser 195	tct Ser	tct Ser	cac His	tca Ser	gct Ala 200	gjå aaa	agg Arg	gac Asp	atg Met	gca Ala 205	gct Ala	gcc Ala	atg Met	625
	tac Tyr 210															646
<21: <21: <21: <21:	1 > 2 2 > 1	421 215 PRT Mus 1	musci	ılus	dome	estio	cus									
<22 <22 <22 <22	1> 1	misc (1).	(64)	5)	n	lono	- 0	DQ12	- 4 7M	6 • Д	cces	sion	שמח	T/EM	BL/GenBan	.k =
	7398		.1 = .	1009.	2; C.	LOHE	_ 0.	K)12	7 / 1-1	o, A	cccs	31011	DDD.	<i>5</i> , <b>2.</b> 1.	- <b>-,</b>	
	7398		= .	1009.	2; C.	ione	- 0	K)12	- 4 71.1	υ, <sub>Γ</sub>			DDD.	<i>3</i> , 2, .	,	
AF0 <40	7398	4 421														
AF0 <40 Ser 1	7398 0>	4 421 Asp	Val	Cys 5	Phe	Ser	Ser	Thr	Thr 10	Val	Pro	Lys	Val	Leu 15	Ala	
AFO <40 Ser 1	7398 0> Val His	4 421 Asp Ile	Val Leu 20	Cys 5 Arg	Phe Asn Cys	Ser	Ser Ala	Thr Ile 25	Thr 10 Ser	Val Phe Met	Pro	Lys Gly Asn	Val Cys 30	Leu 15 Leu	Ala	
AFO <40 Ser 1 Ile	7398 0> Val His	421 Asp Ile Tyr 35	Val Leu 20	Cys 5 Arg Leu	Phe Asn Cys	Ser Gln Val	Ser Ala Phe	Thr Ile 25	Thr 10 Ser	Val Phe Met	Pro Ser Asp	Lys Gly Asn 45	Val Cys 30	Leu 15 Leu Leu	Ala Thr	
AFO <40 Ser 1 Ile Gln Ala	7398 0> Val His Leu Val	4 421 Asp Ile Tyr 35 Met	Val Leu 20 Phe	Cys 5 Arg Leu Tyr	Phe Asn Cys Asp	Ser Gln Val Arg	Ser Ala Phe 40	Thr Ile 25 Ala Val	Thr 10 Ser Asp	Val Phe Met	Pro Ser Asp Cys	Lys Gly Asn 45	Val Cys 30 Phe	Leu 15 Leu Leu	Ala Thr Leu	
AFO <40 Ser 1 Ile Gln Ala Tyr 65	7398 0> Val His Leu Val 50	4 421 Asp Ile Tyr 35 Met	Val Leu 20 Phe Ala	Cys 5 Arg Leu Tyr	Phe Asn Cys Asp Thr	Ser Gln Val Arg 55	Ser Ala Phe 40 Phe	Thr Ile 25 Ala Val	Thr 10 Ser Asp Ala	Val Phe Met Ile	Pro Ser Asp Cys 60	Lys Gly Asn 45 His	Val Cys 30 Phe Pro	Leu Leu Leu Val	Ala Thr Leu His	
AFO <40 Ser 1 Ile Gln Ala Tyr 65 Ser	7398 0> Val His Leu Val 50 Thr	4 421 Asp Ile Tyr 35 Met	Val Leu 20 Phe Ala Lys	Cys 5 Arg Leu Tyr Met Ala 85	Phe Asn Cys Asp Thr 70 Ser	Ser Gln Val Arg 55 His	Ser Ala Phe 40 Phe Gln	Thr Ile 25 Ala Val	Thr 10 Ser Asp Ala Cys Leu 90	Val Phe Met Ile Ala 75	Pro Ser Asp Cys 60	Lys Gly Asn 45 His	Val Cys 30 Phe Pro	Leu Leu Val Leu 95	Ala Thr Leu His	

115 120 125

Glu Leu Met Ile Leu Ala Val Ala Gly Leu Ile Met Leu Ala Pro Phe Val Cys Ile Leu Leu Ser Tyr Ile Leu Ile Ala Cys Ala Ile Leu Lys 150 155 Ile Ser Ser Thr Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Ile Ile Ser Leu Tyr Phe 185 Asn Pro Ser Ser Ser His Ser Ala Gly Arg Asp Met Ala Ala Met 200 Met Tyr Thr Val Val Thr Pro 210 215 <210> 422 <211> 650 <212> DNA <213> Mus musculus domesticus <220> <221> misc\_feature <222> (1)..(650) <223> Taxon = 10092; clone = OR912-47M7; Accession DDBJ/EMBL/GenBank = AF073985 <220> <221> CDS <222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7 <400> 422 c ttt gtg gac atc tgt ttc acc tcc acc act gtc cca aag atg ctg gta Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val 49 aat ata cag act caa agc aag gcc att aca tat gca gac tgt att agc 97 Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala Asp Cys Ile Ser 145 cag atg tct gtc ttc ttg gtt ttt gga gaa ctg gac aac ttt ctc ctg Gln Met Ser Val Phe Leu Val Phe Gly Glu Leu Asp Asn Phe Leu Leu 35 40 193 gct gtg atg gcc tat gac cga tat gtg gct atc tgt cac cca ttg tat Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr 50 55 241 tac aca ttc att gtt aac caa cat ctc tgt ata ctg atg gtt ctg ctg Tyr Thr Phe Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu

tee tog gtt gtt age ate eta cat gee tte tta cag age tea att gta

75

289

Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Se: 85 90	Ser Ile Val 95
cta cag ttg acc ttt tgt gga gat gta aga att ccc cac Leu Gln Leu Thr Phe Cys Gly Asp Val Arg Ile Pro His 100 105	
gag ctt aac cag ctg tct caa ctc aca tgt tca gac agg Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp Ser 115 120 129	Leu Ser Ser
cac ctc ata atg cat ctt gta cct gtt cta ttg gga gcc His Leu Ile Met His Leu Val Pro Val Leu Leu Gly Ala 130 135 140	
agt agt atc ctt tac tct tat ttc aag ata gtg tcc tcc Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser 145 150 155	
atc tcc tca gtt caa ggg aag tac aag gca ttt tct acc Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Th 165 170	
cac ctt tcc att gta tcc tta ttt tat agt aca ggc ct His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly Let 180	
gtc agt tct gct gtg gtc caa agc tct cac tct gct gcc Val Ser Ser Ala Val Val Gln Ser Ser His Ser Ala Ala 195 200 209	a Arg Ala Ser
gtg atg tat act gtg gtc aca cac g Val Met Tyr Thr Val Val Thr His 210 215	650
<210> 423 <211> 216 <212> PRT <213> Mus musculus domesticus	
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Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala As 20 25	p Cys Ile Ser 30
Gln Met Ser Val Phe Leu Val Phe Gly Glu Leu Asp As: 35 40 45	n Phe Leu Leu
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Ser	Trp	Val	Val	Ser 85	Ile	Leu	His	Ala	Phe 90	Leu	Gln	Ser	Ser	Ile 95	Val		
Leu	Gln	Leu	Thr 100	Phe	Cys	Glỵ	Asp	Val 105	Arg	Ile	Pro	His	Phe 110	Phe	Cys		
Glu	Leu	Asn 115	Gln	Leu	Ser	Gln	Leu 120	Thr	Сув	Ser	Asp	Ser 125	Leu	Ser	Ser		
His	Leu 130	Ile	Met	His	Leu	Val 135	Pro	Val	Leu	Leu	Gly 140	Ala	Ile	Ser	Phe		
Ser 145	Ser	Ile	Leu	Tyr	Ser 150	Tyr	Phe	Lys	Ile	Val 155	Ser	Ser	Ile	Cys	Ser 160		
Ile	Ser	Ser	Val	Gln 165	Gly	Lys	Tyr	Lys	Ala 170	Phe	Ser	Thr	Cys	Val 175	Ser		
His	Leu	Ser	Ile 180	Val	Ser	Leu	Phe	Tyr 185	Ser	Thr	Gly	Leu	Gly 190	Val	Tyr		
Val	Ser	Ser 195		Val	Val	Gln	Ser 200	Ser	His	Ser	Ala	Ala 205	Arg	Ala	Ser		
Val	Met 210		Thr	Val	Val	Thr 215	His										
<21 <21 <21 <21	1 > 2 >	424 649 DNA Mus	musc	ulus	dom	esti	cus										
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	1> 2> 3>	CDS (2). Prod TM7	uct	9) = ol	fact	ory	rece	ptor	; re	gion	. bet	ween	tra	nsme	mbrane	domai	ns
c t	he V	ta a	ac a sp I	tc t le C	gt t ys P	tc a he T	cc t hr S	cc a Ser T	hr T	ct g hr V	tc c al F	ca a ro L	ag g ys V	al L	tg gta eu Val 5	4	9
aat Asn	ata Ile	cag Gln	act Thr 20	caa Gln	ago Ser	aag Lys	gcc Ala	att Ile 25	aca Thr	tat Tyr	gca Ala	gac Asp	tgt Cys 30	att Ile	agc Ser	9	7
cag	atg	, tct	gto	ttc	ttg	gtt	ttt	gca	gaa	ttg	gac	aac	ttt	cto	ctg	14	: 5

Gln	Met	Ser 35	Val	Phe	Leu	Val	Phe 40	Ala	Glu	Leu	Asp	Asn 45	Phe	Leu	Leu	
													cca Pro			193
tac Tyr 65	aca Thr	ttc Phe	att Ile	gtt Val	aac Asn 70	caa Gln	cat His	ctc Leu	tgt Cys	ata Ile 75	ctg Leu	atg Met	gtt Val	ctg Leu	ctg Leu 80	241
													tca Ser			289
cta Leu	cag Gln	ttg Leu	acc Thr 100	ttt Phe	tgt Cys	gga Gly	gat Asp	gta Val 105	aaa Lys	att Ile	ccc Pro	cac His	ttc Phe 110	ttc Phe	tgc Cys	337
gag Glu	ctt Leu	aac Asn 115	cag Gln	ctg Leu	tct Ser	caa Gln	ctc Leu 120	aca Thr	tgt Cys	tta Leu	gac Asp	agc Ser 125	ttt Phe	tca Ser	agc Ser	385
cac His	ctc Leu 130	ata Ile	atg Met	aat Asn	ctt Leu	gta Val 135	cct Pro	gtt Val	cta Leu	ttg Leu	gca Ala 140	gtc Val	att Ile	tcc Ser	ttc Phe	433
agt Ser 145	agt Ser	atc Ile	ctt Leu	tac Tyr	tct Ser 150	tat Tyr	ttc Phe	aag Lys	ata Ile	gtg Val 155	tcc Ser	tcc Ser	ata Ile	tgt Cys	tct Ser 160	481
atc Ile	tcc Ser	tca Ser	gtt Val	caa Gln 165	Glà aaa	aag Lys	tac Tyr	aag Lys	gca Ala 170	ttt Phe	tct Ser	aca Thr	tgt Cys	gtc Val 175	tct Ser	529
cac His	ctt Leu	tcc Ser	att Ile 180	gtc Val	ttc Phe	tta Leu	ttt Phe	tat Tyr 185	agt Ser	aca Thr	ggc Gly	ctt Leu	gga Gly 190	gtg Val	tat Tyr	577
gtc Val	agt Ser	tct Ser 195	gct Ala	gtg Val	gtc Val	caa Gln	agc Ser 200	tct Ser	cac His	tct Ser	gct Ala	gca Ala 205	aga Arg	gcc Ala	tct Ser	625
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Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr

Tyr Thr Phe Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu

Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val 85

Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro His Phe Phe Cys 100

Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Leu Asp Ser Phe Ser Ser 120

His Leu Ile Met Asn Leu Val Pro Val Leu Leu Ala Val Ile Ser Phe

Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser 155

Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser 165

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cac ttc ctg	gtg aag ag Val Lys Ar 20	g aag acc g Lys Thr	att tct Ile Ser 25	ttt gct g Phe Ala (	gga tgt tct Gly Cys Ser 30	aca 97 Thr
cag ata gtg Gln Ile Val 35	gtg ttg ct Val Leu Le	t ctg gtc u Leu Val 40	gga tgc Gly Cys	Thr Glu	tgt gca ctg Cys Ala Leu 45	ctg 145 Leu
gca gtg atg Ala Val Met 50	tcc tat ga Ser Tyr As	c cga tat p Arg Tyr 55	gtg gct Val Ala	gtc tgc Val Cys 60	aaa cct ctg Lys Pro Leu	cac 193 His
tac tcc acc Tyr Ser Thr 65	atc atg ac Ile Met Th	r His Trp	cta tgt Leu Cys	gtt cag Val Gln 75	ctg gct gca Leu Ala Ala	ggg 241 Gly 80
tcc tgg gcc Ser Trp Ala	agt ggt gg Ser Gly Al	a ctt gtg a Leu Val	tcc ctg Ser Leu 90	gtg gat Val Asp	acc aca ttc Thr Thr Phe 95	aca 289 Thr
tta cgt ctt Leu Arg Leu	cct tat co Pro Tyr An	ga gga aac g Gly Asr	aat gto Asn Val	att aac Ile Asn	cac ttt ttc His Phe Phe 110	tgt 337 Cys
gaa cct cct Glu Pro Pro 115	gcc ctc ct Ala Leu Lo	g aag cto eu Lys Lev 120	ı Ala Ser	g gca gat Ala Asp	aca tac ago Thr Tyr Ser 125	aca 385 Thr
gag atg gcg Glu Met Ala 130	atc ttt g	ca atg ggt la Met Gly 135	t gtg gta y Val Val	a atc ctc l Ile Leu 140	cta gca cct Leu Ala Pro	gtc 433 Val
tcc ctc atc Ser Leu Ile 145	Leu Thr S	cc tac tgg er Tyr Tr 50	g aac ato p Asn Ilo	e atc tcc e Ile Ser 155	act gta ato Thr Val Ile	c cag 481 e Gln 160
atg cag tct Met Gln Ser	ggg gaa g Gly Glu G 165	ga agg ct ly Arg Le	c aag gte u Lys Va 17	I bue per	acc tgt ggo Thr Cys Gly 17	<i>I</i> — — —
cac ctc att His Leu Ile	gtt gtt g Val Val V 180	tt ctc tt al Leu Ph	c tac gg e Tyr Gl 185	c tca gca y Ser Ala	ata ttt gc Ile Phe Ala 190	c tac 577 a Tyr
atg agg ccc Met Arg Pro 195	Asn Ser I	ag ata at ys Ile Me 20	t Asn GI	a aag gat u Lys Asp	aaa atg at Lys Met Il 205	t tcg 625 e Ser
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Gln Ile Val Val Leu Leu Leu Val Gly Cys Thr Glu Cys Ala Leu Leu

Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Lys Pro Leu His 55

Tyr Ser Thr Ile Met Thr His Trp Leu Cys Val Gln Leu Ala Ala Gly 70

Ser Trp Ala Ser Gly Ala Leu Val Ser Leu Val Asp Thr Thr Phe Thr

Leu Arg Leu Pro Tyr Arg Gly Asn Asn Val Ile Asn His Phe Phe Cys

Glu Pro Pro Ala Leu Leu Lys Leu Ala Ser Ala Asp Thr Tyr Ser Thr

Glu Met Ala Ile Phe Ala Met Gly Val Val Ile Leu Leu Ala Pro Val

Ser Leu Ile Leu Thr Ser Tyr Trp Asn Ile Ile Ser Thr Val Ile Gln 145

Met Gln Ser Gly Glu Gly Arg Leu Lys Val Phe Ser Thr Cys Gly Ser

His Leu Ile Val Val Val Leu Phe Tyr Gly Ser Ala Ile Phe Ala Tyr 180

Met Arg Pro Asn Ser Lys Ile Met Asn Glu Lys Asp Lys Met Ile Ser 200

Val Phe Tyr Ser Ala Val Thr Pro

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aac Asn	atg Met	cag Gln	agc Ser 20	caa Gln	gtt Val	cct Pro	tca Ser	atc Ile 25	ccc Pro	tat Tyr	gca Ala	ggc Gly	tgc Cys 30	ctg Leu	aca Thr	97
caa Gln	atg Met	tac Tyr 35	ttc Phe	ttt Phe	ttg Leu	ttt Phe	ttt Phe 40	gga Gly	gat Asp	ctt Leu	gag Glu	agc Ser 45	ttc Phe	ctc Leu	ctt Leu	145
gtg Val	gcc Ala 50	atg Met	gcc Ala	tat Tyr	gac Asp	cga Arg 55	tat Tyr	gta Val	gcc Ala	atc Ile	tgc Cys 60	ttc Phe	cct Pro	ctt Leu	cat His	193
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act Thr	agg Arg	ttg Leu	tct Ser 100	ttc Phe	tgt Cys	gaa Glu	aac Asn	aat Asn 105	gtg Val	atc Ile	ccc Pro	cat His	ttt Phe 110	ttc Phe	tgt Cys	337
gat Asp	ctg Leu	tct Ser 115	gct Ala	ctg Leu	ctg Leu	aag Lys	ctg Leu 120	gcc Ala	tgc Cys	tct Ser	gat Asp	att Ile 125	cac His	att Ile	aat Asn	385
gaa Glu	ttg Leu 130	gtg Val	ata Ile	ttg Leu	atc Ile	ata Ile 135	gga Gly	Gly aaa	ctt Leu	gtt Val	gtt Val 140	ıте	ctt Leu	cca Pro	ttt Phe	433
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gtc Val	cct Pro	tca Ser	act Thr	cga Arg 165	ggc	atc Ile	cac His	aag Lys	gtc Val 170	Phe	tcc Ser	act Thr	tgt Cys	ggt Gly 175	tct Ser	529
cac His	ctg Leu	tct Ser	gtg Val 180	Val	tca Ser	ctg Leu	ttc Phe	tat Tyr 185	Gly	aca Thr	att Ile	att Ile	ggc Gly 190	Leu	tac Tyr	577
tta Leu	tgt Cys	cca	tct Ser	gct Ala	aat Asn	aac Asn	tct	Thr	cta Leu	aag Lys	gac Asp	act Thr	Val	atg Met	tct Ser	625

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Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His

Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu

Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu

Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys 105 100

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 120

Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe

Leu Leu Val Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 185

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Leu Met Tyr Thr Val Val Thr Pro 210 215

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gtctaagaga agaatgagat ttcaaaagga atggatacag agaaggtatg gtcatattca
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cagagacett tetgaatgat cagaacttag tgtaaccact gaaaaatgtt gagaagtgaa
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Ser Gly Val Phe Gln Tyr Pro Glu His Gln Pro Met Leu Phe Gly Leu
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                                                                       684
Phe Leu Leu Met Phe Val Val Ala Val Leu Gly Asn Leu Leu Ile Ile
ctg gcc gtc agc att gac tct cac ctg cat act ccc atg tac ttc ttt
                                                                       732
Leu Ala Val Ser Ile Asp Ser His Leu His Thr Pro Met Tyr Phe Phe
                                 55
             50
                                                                       780
 cta tot aac ctg too ttt tot gac att ggt tto atc tot aca act gto
 Leu Ser Asn Leu Ser Phe Ser Asp Ile Gly Phe Ile Ser Thr Thr Val
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 cct aag atg ttg gtg aat atc caa aca cag agc aag tcc atc tcc tat
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Pro Lys Met Leu Val Asn Ile Gln Thr Gln Ser Lys Ser Ile Ser Tyr

85

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gac a Asp '	aca Thr	ctt Leu	ctc Leu	ctc Leu 115	acc Thr	gtg Val	atg Met	gcc Ala	tat Tyr 120	gac Asp	cga Arg	ttt Phe	gtg Val	gcc Ala 125	atc Ile	924
tgt ( Cys )	cac His	cca Pro	ctt Leu 130	cac His	tat Tyr	tca Ser	gtc Val	att Ile 135	atg Met	aat Asn	cct Pro	caa Gln	cta Leu 140	agt Ser	ggt Gly	972
ttg ( Leu )	cta Leu	gtt Val 145	ctt Leu	gta Val	tca Ser	tgg Trp	ttt Phe 150	att Ile	agc Ser	ttt Phe	tca Ser	tat Tyr 155	tct Ser	ctg Leu	ata Ile	1020
cag Gln	agt Ser 160	cta Leu	ttg Leu	atg Met	ctg Leu	cgg Arg 165	ttg Leu	tcc Ser	ttc Phe	tgt Cys	aca Thr 170	aat Asn	cag Gln	ata Ile	att Ile	1068
aaa Lys 175	cac His	ttt Phe	tac Tyr	tgt Cys	gaa Glu 180	tat Tyr	gcc Ala	aaa Lys	gcc Ala	ctc Leu 185	act Thr	ata Ile	gcc Ala	tgc Cys	tca Ser 190	1116
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aca Thr	ctt Leu	999 305	Arg	ata Ile	ctt Leu	ctt Leu	tta Leu 310	aag Lys	tga	taa	tttc	act	ggtt	ttag	ac	1502
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cga	cata	ttt	cttt	actt	ca g	rtaca	aagt	c ta	catt	tcag	g cat	gcca	ata	taac	cattca	1742
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Leu	Met	Phe 35	Val	Val	Ala	Val	Leu 40	Gly	Asn	Leu	Leu	Ile 45	Ile	Leu	Ala	
Val	Ser 50	Ile	Asp	Ser	His	Leu 55	His	Thr	Pro	Met	Tyr 60	Phe	Phe	Leu	Ser	
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Cys	Ile	Thr	Gln 100	Ile	Tyr	Phe	Phe	Met 105	Leu	Phe	Gly	Gly	Met 110	Asp	Thr	
Leu	Leu	Leu 115	Thr	Val	Met	Ala	Tyr 120	Asp	Arg	Phe	Val	Ala 125	Ile	Сув	His	
Pro	Leu 130	His	Tyr	Ser	Val	Ile 135	Met	Asn	Pro	Gln	Leu 140	Ser	Gly	Leu	Leu	
Val 145	Leu	Val	Ser	Trp	Phe 150		Ser	Phe	Ser	Tyr 155	Ser	Leu	Ile	Gln	Ser 160	
Leu	Leu	Met	Leu	Arg 165	Leu	Ser	Phe	Суз	Thr 170	Asn	Gln	Ile	Ile	Lys 175	His	
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IJ





Leu Ile Asn His Ile Leu Leu Tyr Ile Val Ile Trp Val Leu Gly Phe 195  $^{1}$ , 200 205

Ile Pro Phe Ser Gly Ile Leu Tyr Ser Tyr Tyr Lys Ile Phe Ser Ser 210 215 220

Ile Leu Arg Ile Pro Ser Thr Asp Gly Lys Tyr Lys Ala Phe Ser Thr 225 230 235 235

Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu 245 250 255

Ser Val Tyr Leu Ser Ser Asp Ala Thr Ser Ser Ser Gly Lys Gly Val 260 265 270

Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe 275 280 285

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